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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 01:57:46 ; Search time 2513.97 Seconds
(without alignments)
705.652 Million cell updates/sec

Title: US-09-016-869A-1
Perfect score: 994
Sequence: 1 CGGAGAGGGGAGACAGAC.....CATTCACTCACTCAAAAAA 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 972840 seqs, 892348106 residues 1945680
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 79: gb_htg30.*
- 80: gb_htg31.*
- 81: gb_vil.*
- 82: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query %	Match	Length	DB	ID	Description
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3	943.8	94.9	94.9	947	5	AR037526		AR037526 Sequence
4	943.8	94.9	94.9	947	5	AR062806		AR062806 Sequence
5	943.8	94.9	94.9	947	5	I41180		I41180 Sequence 36
6	801	80.6	1017	10	HS026727			U26727 Human p16IN
7	801	80.6	1131	5	AR001325			AR001325 Sequence
8	801	80.6	1131	5	AR037505			AR037505 Sequence
9	801	80.6	1131	5	AR062785			AR062785 Sequence
10	801	80.6	1131	5	I41159			I41159 Sequence 13
11	705.4	71.0	1420	5	I67718			I67718 Sequence 1
12	551.2	55.5	905	10	HS038945			U38945 Human hypot
13	489.2	49.2	520	39	S69822S2			S69824 Homo sapien
14	489.2	49.2	34669	39	AC000048			AC000048 Homo sapi
15	467.8	47.1	471	5	AR001314			AR001314 Sequence
16	467.8	47.1	471	5	AR037494			AR037494 Sequence
17	467.8	47.1	471	5	AR062774			AR062774 Sequence
18	467.8	47.1	471	5	I41148			I41148 Sequence 1
19	379	38.1	400	13	GI3475			GI3475 human STS S
20	358.6	36.1	793	39	AF115544			AF115544 Homo sapi
21	330	33.2	660	11	S78535			S78535 tumor suppr
22	310.4	31.2	457	39	S69804			S69804 MTS1-multip
23	310.4	31.2	540	39	S69822S1			S69822 Homo sapien
24	310.4	31.2	1187	5	AR001316			AR001316 Sequence


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RESULT 2
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LOCUS AR001346 947 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 36 from patent US 5739027.
ACCESSION AR001346
VERSION AR001346.1 GI:3963413
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 947)
AUTHORS Kamb,A.
TITLE MTS1E1.beta. gene
JOURNAL Patent: US 5739027-A 36 14-APR-1998;
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BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

Query Match 94.9%; Score 943.8; DB 5; Length 947;
Best Local Similarity 99.8%; Pred. No. 7.3e-151;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 161 CCGAATAGTTACGGTCGGAGGCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGCGG 220
Db 121 CCGAATAGTTACGGTCGGAGGCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGCGG 180
Qy 221 GAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCGGACCCCGCCACTCTACCCGA 280
Db 181 GAGCTGCTGCTCCACGGCGGAGCCCAACTGCGCGGACCCCGCCACTCTACCCGA 240
Qy 281 CCCGTGCACGAGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGCACCGGGCC 340
Db 241 CCCGTGCACGAGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGCACCGGGCC 300
Qy 341 GGGCGCGGCTGGAGCTGGCGGATCGCTGGGGCCGCTCTGCCGCTGGACCTGGCTGAGGAG 400
Db 301 GGGCGCGGCTGGAGCTGGCGGATCGCTGGGGCCGCTCTGCCGCTGGACCTGGCTGAGGAG 360
Qy 401 CTGGGCCATCCGATGTCGACAGTACCTGCGCGCGGCTGGCGGGGGACACAGAGGCACT 460
Db 361 CTGGGCCATCCGATGTCGACAGTACCTGCGCGCGGCTGGCGGGGGACACAGAGGCACT 420
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Db 421 AACCATGCCCGCATAGATGCCCGGAGAGTCCCTAGACATCCCGATTTGAAGAACAG 480
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RESULT 3
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LOCUS AR037526 947 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 36 from patent US 5801236.
ACCESSION AR037526
VERSION AR037526.1 GI:5955382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 947)
AUTHORS Kamb,A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 36 01-SEP-1998;
FEATURES
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BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

Query Match 94.9%; Score 943.8; DB 5; Length 947;
Best Local Similarity 99.8%; Pred. No. 7.3e-151;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 41 ATGGATCCGGGGCGGGAGCAGATGAGCGCTTCGGGTGACTGCTGCCACGCCCGCG 100
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Qy 341 GGGCGCGGCTGGAGCTGGCGGATCGCTGGGGCCGCTCTGCCGCTGGACCTGGCTGAGGAG 400
Db 301 GGGCGCGGCTGGAGCTGGCGGATCGCTGGGGCCGCTCTGCCGCTGGACCTGGCTGAGGAG 360
Qy 401 CTGGGCCATCCGATGTCGACAGTACCTGCGCGCGGCTGGCGGGGGACACAGAGGCACT 460
Db 361 CTGGGCCATCCGATGTCGACAGTACCTGCGCGCGGCTGGCGGGGGACACAGAGGCACT 420
Qy 461 AACCATGCCCGCATAGATGCCCGGAGAGTCCCTAGACATCCCGATTTGAAGAACAG 520
Db 421 AACCATGCCCGCATAGATGCCCGGAGAGTCCCTAGACATCCCGATTTGAAGAACAG 480
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Db 521 AGAGGCTCTGAGAACCTCGGGAAACTTAGATCATCAGTCACCGAAGGTCTCTACAGGGCC 540
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Kamb,A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 13 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..1131
BASE COUNT 232 a 327 c 343 g 229 t
ORIGIN

Query Match 80.6%; Score 801; DB 5; Length 1131;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CCAGGTCATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCCACGGCGCGGA 246
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QY 247 GCCCACTGGCGGACCCCGCCACTCTCACCCGACCGCTGCACGACGCTGCCCGGGAGGG 306
DB 391 GCCCACTGGCGGACCCCGCCACTCTCACCCGACCGCTGCACGACGCTGCCCGGGAGGG 450

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QY 667 GATATAAGCCTTCCCGACATACCGTAATGTCATTTATATATATATATATATATCTTA 726
DB 811 GATATAAGCCTTCCCGACATACCGTAATGTCATTTATATATATATATATATCTTA 870

QY 727 TAAAAATGTAAAAAGAAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTTCTTGA 786
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QY 907 TGGCTCTCTTGTAGTCACACTGTAGCAAAATGGCAGACCAAGCTCAATATAAAATAAA 966
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LOCUS Sequence 13 from patent US 5843756.
DEFINITION AR062785
ACCESSION AR062785
VERSION AR062785.1 GI:5990476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 13 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..1131
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ORIGIN

Query Match 80.6%; Score 801; DB 5; Length 1131;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CCAGGTCATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCCACGGCGCGGA 246
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QY 427 CTTCTCTGACACGCTGGTGTGCTGCACCGCGCGGGCGGGCTGGACGTGCCCGATGC 486
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QY 667 GATATAAGCCTTCCCGACATACCGTAATGTCATTTATATATATATATATATCTTA 726
DB 811 GATATAAGCCTTCCCGACATACCGTAATGTCATTTATATATATATATATATCTTA 870

QY 727 TAAAAATGTAAAAAGAAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTTCTTGA 786
DB 871 TAAAAATGTAAAAAGAAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTTCTTGA 930

QY 787 GTGAGCACTCAGCCCTAAGCGCACATTCATGTGGGCAATTCCTGCGAGCCTCCAGCCT 846
DB 931 GTGAGCACTCAGCCCTAAGCGCACATTCATGTGGGCAATTCCTGCGAGCCTCCAGCCT 990

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QY 907 TGGCTCTCTTGTAGTCACACTGTAGCAAAATGGCAGACCAAGCTCAATATAAAATAAA 966
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RESULT 10
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DEFINITION Sequence 13 from patent US 5624819.
ACCESSION I41159
VERSION I41159.1 GI:2081749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germ-line mutations in the MTS gene
JOURNAL Patent: US 5624819-A 13 29-APR-1997;
FEATURES Location/Qualifiers
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BASE COUNT 232 a 327 c 343 g 229 t
ORIGIN

Query Match 80.6%; Score 801; DB 5; Length 1131;
Best Local Similarity 100.0%; Pred. No. 1.2e-126;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 CCAGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCAGCGCGCGGA 246
Db 331 CCAGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCAGCGCGCGGA 390
Qy 247 GCCCAACTGCGCGACCGCGGCACATCTACCGACCGCGTGCACGACGCTGCCCGGAGGG 306
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Qy 547 TTAGATCATCAGTACCGNAGTCTTACAGGCGCACACTGCCCGCGCACAAACCCACC 606
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Qy 607 CGCTTTCTGAGTTTCATTAGAAAATAGAGCTTTTAAAAATGCTGCTGCTTTTAAACGTA 666
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Qy 667 GATATAAGCTTCCCGCCACTACCGTAAATGTCCATTTATATATATATATATATATTTTA 726
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Qy 907 TGGCTTCTCTTGGTACACACTGCTAGCAATGGCAGAACCAAGCTCAAAATAAAATAAA 966
Db 1051 TGGCTTCTCTTGGTACACACTGCTAGCAATGGCAGAACCAAGCTCAAAATAAAATAAA 1110
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RESULT 11
167718
LOCUS I67718 1420 bp DNA PAT 30-DEC-1997
DEFINITION Sequence 1 from patent US 5672508.
ACCESSION I67718
VERSION I67718.1 GI:2731253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1420)
AUTHORS Gyuris,J., Lamphere,L. and Beach,D.
TITLE Inhibitors of cell-cycle progression, and uses related thereto
JOURNAL Patent: US 5672508-A 1 30-SEP-1997;
FEATURES Location/Qualifiers
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BASE COUNT 322 a 410 c 458 g 230 t
ORIGIN

Query Match 71.0%; Score 705.4; DB 5; Length 1420;
Best Local Similarity 99.2%; Pred. No. 1.9e-110;
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Qy 212 CGAGTGGCGGAGCTGCTGCTCTCCAGCGCGGAGCCCAACTGCGCGACCCGCCACT 271
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Qy 272 CTCACCGACCCGCTGCAGACGCTGCCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTG 331
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Qy 332 CACCGCGCGGGCGCGCTGAGCTGCGCGATCGCTGGGCGCGTCTGCGCGTGGACCTG 391
Db 1000 CACCGCGCGGGCGCGCTGAGCTGCGCGATCGCTGGGCGCGTCTGCGCGTGGACCTG 1059
Qy 392 GCTGAGGAGCTGGGCGCATTCGCGAGTGTGCGACGTAACCTGCGCGGGGCTGCGGGGGACC 451
Db 1060 GCTGAGGAGCTGGGCGCATTCGCGAGTGTGCGACGTAACCTGCGCGGGGCTGCGGGGGACC 1119

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QY 452 AGAGGAGTAACCATGCCCCGCGATAGATCCGCGGAAGTCCCTCAGACATCCCCGATTGA 511
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QY 572 TACAGGGCACAACTGCCCCGCCACCAACCCACCCGCTTCGTAAGTTTCATTAGAAA 631
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RESULT 12
HSU38945
LOCUS HSU38945 905 bp mRNA PRI 05-JUN-1996
DEFINITION Human hypothetical 18.1 kDa protein (CDKN2A) mRNA, complete cds.
ACCESSION U38945
VERSION U38945.1 GI:1353569
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Linnenbach,A.J.
TITLE mRNA isoform with alternate first exon-encoded sequences at the
cyclin-dependent kinase inhibitor 2 (p16INK4/MTSL) locus and
mapping analysis of the region by using long-PCR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 905)
AUTHORS Linnenbach,A.J.
TITLE Direct Submission
JOURNAL Submitted (19-OCT-1995) Alban J. Linnenbach, The Wistar Institute,
3601 Spruce Street, Philadelphia, PA 19104, USA
FEATURES
location/Qualifiers
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38..559
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reading frame"
/codon_start=1
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Best Local Similarity 99.5%; Pred. No. 2.7e-84;
Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 187 CCAGTCTATGATGGGCGAGCCGCGAGTGGCGGAGCTGCTGCTCCACGGCGCGGA 246
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QY 247 GCCCAACTGCGCGGACCCCGCCACTCTCACCAGACCCGCTGCACGACGCTGCCGGGAGGG 306
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QY 307 CTTCTGGACACGCTGGTGGTCTGCACCGGCGCGGGCGGCTGGAGCGTGGCGGATGC 366
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QY 367 CTGGGCGCTCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTA 426
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Db 530 CTGGGCGCTCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGCGATGTCGACGGTA 589
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QY 427 CTTGCGCGGCTGCGGGGGCACCAGAGGAGTAAACCATGCCCGCATAGATGCCCGGA 486
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QY 547 TTAGATCATCATCAGTACCGAAGTCTTACAGGCGCCACAACTGCCCGCCACAAACCCACCC 606
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QY 607 CGCTTTCTAGTTTTCATTAGAAAATAGAGCTTTTAAATAATGCTCCTGCTTTTACGTA 666
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Db 770 CGCTTTCTAGTTTTCATTAGAAAATAGAGCTTTTAAATAATGCTCCTGCTTTTACGTA 829
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QY 667 GATATAAGCCTTCCCGCTACCGTAATGTCATATATATATATATATATATATATATCTTA 726
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Db 830 GATATAAGCCTTCCCGCTACCGTAATGTCATATATATATATATATATATATATATCTTA 889
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QY 727 TAAAAATGTAATAAAG 742
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Db 890 TAAAAATGTAATAAAG 905
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RESULT 13
S69822S2
LOCUS S69822S2 520 bp DNA PRI 05-APR-1999
DEFINITION Homo sapiens CDK4i exon, partial sequence; and cyclin-dependent
kinase 4 inhibitor (CDK4i) gene, partial cds.
ACCESSION S69824
VERSION S69824.1 GI:546701
KEYWORDS
SEGMENT 2 of 2
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Nobori,T., Mura,K., Wu,D.J., Lois,A., Takabayashi,K. and
Carson,D.A.
TITLE Deletions of the cyclin-dependent kinase-4 inhibitor gene in
multiple human cancers
JOURNAL Nature 368 (6473), 753-756 (1994)
MEDLINE 9403288
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 146822] from the original journal article.
FEATURES
location/Qualifiers
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/cell_type="melanoma"
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RESULT 15
AR001314 AR001314 471 bp DNA PAT 04-DEC-1998
LOCUS Sequence 1 from patent US 5739027.
DEFINITION AR001314
ACCESSION AR001314
VERSION AR001314.1 GI:3963381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kamb,A.
TITLE MTS1E1.beta. gene
JOURNAL Patent: US 5739027-A 1 14-APR-1998;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 47.1%; Score 467.8; DB 5; Length 471;
Best Local Similarity 99.6%; Pred. No. 3.8e-70;
Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 ATGGAGCCGGCGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGCGCCGCG 60
QY 101 GCCCGGGGTCGGGTAGAGAGGTGGGGGCGCTGCTGGAGCGGTGGCGTGCACACGCA 160
Db 61 GCCCGGGGTCGGGTAGAGAGGTGGGGGCGCTGCTGGAGCGGTGGCGTGCACACGCA 120
QY 161 CCGAATAGTACGGTCGGAGCGCATCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGT 220
Db 121 CCGAATAGTACGGTCGGAGCGCATCCAGGTCCAGGTCCAGGTCCAGGTCCAGGTCCAGGT 180
QY 221 GAGCTGCTGCTCTCCACGGCGCGGAGCCCAACTGGCGGACCCCGCCACTCTCACCCTGA 280
Db 181 GAGCTGCTGCTCTCCACGGCGCGGAGCCCAACTGGCGGACCCCGCCACTCTCACCCTGA 240
QY 281 CCGGTGACGAGCGCTGCCGGGAGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGG 340
Db 241 CCGGTGACGAGCGCTGCCGGGAGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGG 300
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Db 301 GGGGCGCGGCTGGACGTGCGCGATGCTGGGCGCGCTTCGCCGTGGACCTGGCTGAGGAG 360
QY 401 CTGGGCGCATCGCGATGTGCGACGGTACCTGGCGGGGCTGGCGGGGCGCACAGAGGCAGT 460
Db 361 CTGGGCGCATCGCGATGTGCGACGGTACCTGGCGGGGCTGGCGGGGCGCACAGAGGCAGT 420
QY 461 AACCATGCCCGCATAGATGCCGGAAGGTCCCTCAGACATCCCGGATTGA 511
Db 421 AACCATGCCCGCATAGATGCCGGAAGGTCCCTCAGACATCCCGGATTGA 471

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Job time: 14831 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 02:31:23 ; Search time 107.17 Seconds
(without alignments)
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Title: US-09-016-869A-1
Perfect score: 994
Sequence: 1 CGGAGAGGGGAGACAGAC.....CATTCTACTCAAAAAA 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	994	100.0	994	1 T02962	Cell-cycle regulat
2	982.2	98.8	987	1 T60951	Tumour suppressor
3	945.4	95.1	947	1 T00747	Multiple tumour su
4	943.8	94.9	947	1 T72311	Human multiple tum
5	943.8	94.9	947	1 V11270	Human MTS1 cDNA va
6	943.8	94.9	947	1 V53851	Coding sequence 3
7	943.8	94.9	947	1 V70515	cDNA encoding a hu
8	937.6	94.3	948	1 Q63491	Inhibitor of cycli
9	801	80.6	1131	1 T00744	Multiple tumour su
10	801	80.6	1131	1 Q99164	Human MTS polypept
11	801	80.6	1131	1 T69780	Human multiple tum
12	801	80.6	1131	1 V11249	Human MTS1E1-beta
13	801	80.6	1131	1 V53830	Coding sequence 1
14	801	80.6	1131	1 V70594	cDNA encoding a hu
15	705.4	71.0	1420	1 T74051	CDK inhibitory fus
16	705.4	71.0	1420	1 X26220	Human p27-p16 fusl
17	489.2	49.2	4286	1 T15158	CDK4i cyclin-depen
18	468.8	47.2	782	1 X26234	Truncated p27/p16
19	468.8	47.2	1073	1 X26232	Truncated p27/p16
20	467.8	47.1	471	1 V11238	Human MTS1 cDNA. D
21	467.8	47.1	471	1 V53819	Nucleotide sequenc
22	467.8	47.1	471	1 V70583	cDNA encoding a hu
23	467.4	47.0	737	1 X26233	Truncated p27/p16
24	467.4	47.0	1028	1 X26231	Truncated p27/p16
25	467.4	47.0	1121	1 X26235	Human p16p27 fusio
26	466.2	46.9	471	1 T69768	Human multiple tum
27	466.2	46.9	471	1 T69769	Human multiple tum
28	463.8	46.7	1143	1 T74052	CDK inhibitory fus
29	463.8	46.7	1143	1 X26223	Human p16(GS)p27 f
30	463.4	46.6	1098	1 T74053	CDK inhibitory fus
31	463.4	46.6	1098	1 X26224	Human p16p27 fusio
32	447	45.0	447	1 T00736	Multiple tumour su
33	447	45.0	447	1 Q99158	Human multiple tum

34	445.4	44.8	447	1 T00749	Multiple tumour su
35	445.4	44.8	447	1 T00750	Multiple tumour su
36	310.4	31.2	1187	1 T00739	Multiple tumour su
37	310.4	31.2	1187	1 V11240	Human MTS1 genomic
38	310.4	31.2	1187	1 V53821	Coding sequence 2
39	310.4	31.2	1187	1 V70585	Human multiple tum
40	305.6	30.7	1185	1 Q99167	Human MTS1 DNA inc
41	300.4	30.2	306	1 T15155	CDK4i' exon from c
42	285.6	28.7	751	1 T00745	Multiple tumour su
43	285.6	28.7	751	1 Q99165	Human multiple tum
44	285.6	28.7	751	1 T69781	Human multiple tum
45	285.6	28.7	751	1 V11250	Human MTS2 cDNA. D

ALIGNMENTS

RESULT 1					
T02962					
ID	T02962	standard; cDNA; 994 BP.			
AC	T02962;				
DT	01-MAR-1996	(first entry)			
DE	Cell-cycle regulatory protein p16 cDNA.				
KW	Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;				
KW	CCR: gene therapy; transgenic animal; cancer; cell proliferation;				
SS; ds.					
OS	Homo sapiens.				
FH Key	Location/Qualifiers				
FT cds	41..511				
FT	/*tag= a				
PN	W09528483-A1.				
PD	26-OCT-1995.				
PF	14-APR-1995; U04636.				
PR	14-APR-1994; US-227371.				
PR	25-MAY-1994; US-248812.				
PR	14-SEP-1994; US-306511.				
PR	29-NOV-1994; US-346147.				
PA	(COLD-) COLD SPRING HARBOR LAB.				
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;				
DR	WPI; 95-373798/48.				
DR	P-P6DB; R85116.				
PT	New cell cycle regulating proteins bind to cyclin dependent kinase -				
PT	and related nucleic acids, antibodies etc., used in diagnosis and				
PT	therapy of abnormal cell proliferation, degeneration etc.				
PS	Claim 43; Page 76-77; 109pp; English.				
CC	cDNA (T02962) coding for the human cell-cycle regulatory (CCR)				
CC	protein p16 (R85116) was isolated using a 2-hybrid screening assay				
CC	in Saccharomyces cerevisiae. The p16 gene was mapped to chromosome				
CC	9p21-22. The isolated cDNA can be used: to detect mutations in				
CC	CCR genes that lead to cell proliferation; to breed transgenic				
CC	animals to study cellular disorders involving CCR allele				
CC	mutation/misexpression; and to correct CCR-deficient cells				
CC	(gene therapy).				
SC	Sequence 994 BP; 225 A; 279 C; 293 G; 197 T;				

Query Match	100.0%;	Score 994;	DB 1;	Length 994;
Best Local Similarity	100.0%;	Pred. No. 2.3e-214;		
Matches 994;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	CAGCATGGAGCCCTTCGGCTGACTGGCTGGCCAGCGCGGGGGGAGCAGCATGATCCGGCGGGGAG	120	
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Db	121	GGTGGGGGGCTGCTGGAGCGGCTGGCGTCCCAACGACCGCAATAGTTACGGTCGGAG	180	
QY	181	GCCGATCCAGGTCATGATGATGGGAGCGGCCCGGAGTGGCGGAGCTGCTGCTCCACGG	240	

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Qy 301 GGAGGGCTTCCTGGACACGCTGGTGGTCTGACCGGCGCGGGCGGCTGGAGCTGG 360
Db 301 GGAGGGCTTCCTGGACACGCTGGTGGTCTGACCGGCGCGGGCGGCTGGAGCTGG 360
Qy 361 CGATGCTGGGGCCCTGCGCGTGGAGCTGGCTGAGAGCTGGGCGCATCGGATGTCG 420
Db 361 CGATGCTGGGGCCCTGCGCGTGGAGCTGGCTGAGAGCTGGGCGCATCGGATGTCG 420
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Db 421 ACGGTACTGCGCGGCTGCGGGGGGACAGAGGCTGACCTGCGCGCATAGATGC 480
Qy 481 CCGGAAGTCCCTCAGACATCCCGATTCGATGAAAGAACAGAGGCTCTGAGAACCTCG 540
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Db 541 GGAACCTTAGATCATCAGTACCGAGGCTCTACAGGGCCACACTGCCCCGCCACAC 600
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Db 661 AACGTAGATATAAGGCTTCCTCCGACATCCGTAATGTCATTTATATATATATA 720
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Db 721 TTCTTATAAATGTAAGGCTTCCTCCGACATCCGTAATGTCATTTATATATATA 780
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Db 901 GGTACTGGCTTCTTGTGAGTACACTGCTAGCAATGCGAGAACCAAGCTCAATATA 960
Qy 961 AATAAATATTTTTCATTCATCTCAAAAAA 994
Db 961 AATAAATATTTTTCATTCATCTCAAAAAA 994

RESULT 2
ID T60951 standard; DNA; 987 BP.
AC T60951;
DT 28-OCT-1997 (first entry)
DE Tumour suppressor p16 coding sequence.
KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
KW anti-angiogenic activity; hyperproliferative disorder; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 41..511
FT /*tag= a
FT /product= Tumour suppressor p16
FN WO9703635-A2.
PD 06-FEB-1997.
PF 17-JUL-1996; U11787.
```

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PR 17-JUL-1995; US-502881.
PA (TEXA ) UNIV TEXAS SYSTEM.
PI Jin X, Roth J;
DR WPI; 97-132336/12.
DR P-PSDB: W10627.
PT Expression construct contg. DNA for tumour suppressor p16 - to
PT restore p16 activity to transformed cells, useful for treating lung
PT or bladder cancer or melanoma
PS Disclosure; Fig 1a; 92pp; English.
CC This sequence represents the coding sequence for the tumour suppressor
CC p16. This sequence is joined to a promoter functional in eukaryotic cells
CC and used in the expression construct of the invention. p16 is an
CC inhibitory subunit, which is involved in the control of cyclin-dependent
CC kinase 4 activity, and functions as a tumour suppressor. By detecting
CC this sequence or the encoded protein, cancer cells can be detected. When
CC the nucleic acid molecule is in the sense orientation, the expression
CC construct can be used to restore p16 function in a cell, particularly by
CC reversing the transformed phenotype in tumours, especially lung or
CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
CC nucleic acid molecule is inserted in the antisense orientation, the
CC expression construct inhibits p16 function. Reduced or increased levels
CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
CC or immunoassay.
SQ Sequence 987 BP; 219 A; 279 C; 295 G; 194 T;

Query Match 98.8%; Score 982.2; DB 1; Length 987;
Best Local Similarity 99.7%; Pred. No. 1e-211; 3; Indels 0; Gaps 0;
Matches 984; Conservative 0; Mismatches 3;

Qy 1 CGGAGAGGGGAGAACAGACAGACGGCGGGGAGCAGCAGTGGATCCGCGCGGGGAG 60
Db 1 CGGAGAGGGGAGAACAGACAGACGGCGGGGAGCAGCAGTGGATCCGCGCGGGGAG 60
Qy 61 CAGCATGGAGGCTTCGCTGACTGGCTGGCCACGGCGCGGGCGGGGCTGGGTAGAGGA 120
Db 61 CAGCATGGAGGCTTCGCTGACTGGCTGGCCACGGCGCGGGCGGGGCTGGGTAGAGGA 120
Qy 121 GGTGCGGGCGCTGCTGGAGCGGTGGCGCTGCCAAGCCAGCAATAGTTACGGTCCGAG 180
Db 121 GGTGCGGGCGCTGCTGGAGCGGTGGCGCTGCCAAGCCAGCAATAGTTACGGTCCGAG 180
Qy 181 GCCGATCCAGGTCAATGATGATGGCAGCGCCGAGTGGCGGAGCTGTGTCTCCACGG 240
Db 181 GCCGATCCAGGTCAATGATGATGGCAGCGCCGAGTGGCGGAGCTGTGTCTCCACGG 240
Qy 241 CGCGGAGCCCAACTGCGCGGACCCCGCCACTCTCACCGGCGCGGCTGCACGAGCTGCCG 300
Db 241 CGCGGAGCCCAACTGCGCGGACCCCGCCACTCTCACCGGCGCGGCTGCACGAGCTGCCG 300
Qy 301 GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Db 301 GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Qy 361 CGATGCTGGGGCCCTGCGCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 420
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Qy 421 ACGGTACTGCGCGGCTGCGGGGGGACAGAGGCTGACCTGCGCGCATAGATGC 480
Db 421 ACGGTACTGCGCGGCTGCGGGGGGACAGAGGCTGACCTGCGCGCATAGATGC 480
Qy 481 CCGGAAGTCCCTCAGACATCCCGGATTCGATGAAAGAACAGAGGCTCTGAGAACCTCG 540
Db 481 CCGGAAGTCCCTCAGACATCCCGGATTCGATGAAAGAACAGAGGCTCTGAGAACCTCG 540
Qy 541 GGAACCTTAGATCATCAGTACCGAGGCTCTACAGGGCCACACTGCCCCGCCACAC 600
Db 541 GGAACCTTAGATCATCAGTACCGAGGCTCTACAGGGCCACACTGCCCCGCCACAC 600
Qy 601 CCACCCCGCTTCGCTAGTATTTTATTTAGAAATAGAGCTTTTAAATGTCTGCTTTT 660
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Db	601	 CCACCCGCCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGTCTGCCTTT	660
Qy	661	AACGTAGATATAAGCCCTCCCCCACTACCGTAAATGCCATTATATCATTTTTTATATA	720
Db	661	AACGTAGATATAAGCCCTCCCCCACTACCGTAAATGCCATTATATCATTTTTTATATA	720
Qy	721	TTCTRTTAAAAATGTAAAAAAGAAAAACACCGCTCTTCGCCCTTTTCACTGTGTGGAGTTT	780
Db	721	TTCTTTATAAAAAATGTAAAAAAGAAAAACACCGCTCTTCGCCCTTTTCACTGTGTGGAGTTT	780
Qy	781	TCTGGAGTGAGCACTACGCGCTTAAGCGCACATTCATGTGGGCATTTCTTGGAGGCTCG	840
Db	781	TC TGGAGTGAGCACTACGCGCTTAAGCGCACATTCATGTGGGCATTTCTTGGAGGCTCG	840
Qy	841	CAGCCTCCGGAAGGTGCGACTTCATGACAAAGCATTTTGTGAACATAGGGAAGCTCAGGGG	900
Db	841	CAGCCTCCGGAAGGTGCGACTTCATGACAAAGCATTTTGTGAACATAGGGAAGCTCAGGGG	900
Qy	901	GGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAATGGCAGAACCAAGCTCAATAAA	960
Db	901	GGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAATGGCAGAACCAAGCTCAATAAA	960
Qy	961	AATAAAATATTTTCATTCAATTCACCTC	987
Db	961	AATAAAATATTTTCATTCAATTCACCTC	987

RESULT 3

T00747	standard; cDNA; 947 BP.
ID	T00747;
AC	08-MAY-1996 (first entry)
DE	Multiple tumour suppressor 1 (MTS1) cDNA.
DT	Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW	predisposition; melanoma; lymphoma; prognosis;
KW	pancreas; breast; thyroid; ds.
KW	Homo sapiens.
OS	
FH	Key
FT	Location/Qualifiers
FT	151
FT	/tag= a
FT	/note= "splice site acceptor"
FT	458
FT	/tag= b
FT	/note= "splice site acceptor"
PN	WO9525813-A1.
PD	28-SEP-1995.
PF	17-MAR-1995. UO3537.
PR	18-MAR-1994; US-214582.
PR	18-MAR-1994; US-215087.
PR	18-MAR-1994; US-215086.
PR	14-APR-1994; US-227369.
PR	01-JUN-1994; US-251938.
PA	(MYRI-) MYRIAD GENETICS INC.
PA	(UTAH) UNIV UTAH RES FOUND.
PI	Cannon-Albright LA, Kamb A,
DR	WT1: 95-344636/44.
PT	Detecting polymorphism associated with cancer pre-disposition - also
PT	DNA, vectors and host cells e.g. for gene or protein replacement
PT	therapy and drug screening
PS	Disclosure; Pages 111-112; 148pp; English.
CC	An individual can be diagnosed as having a predisposition to cancer
CC	by detecting an alteration in the wild type multiple tumour
CC	suppresser (MTS) gene, using gene probes which hybridise to the MTS1
CC	cDNA T00747. The above assay can also be used in the diagnosis and
CC	prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and
CC	thyroid cancers, etc.
SQ	Sequence 947 BP; 207 A; 271 C; 273 G; 196 T;

DECEMBER 1964

RESULTS	4
T72311	
ID	T72311 standard; cDNA; 947 bp.
AC	T72311
DE	Human multiple tumour suppressor gene 1.
DE	Human multiple tumour suppressor gene 1.
DE	Human multiple tumour suppressor gene 1.
KW	Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ds.

Db 1 ATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGCGCG 60
QY 101 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 160
Db 61 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 120
QY 161 CGCAATAGTACGGTGGAGGCGCATCCAGGTATGATGATGGCAGCGCGAGTGGCG 220
Db 121 CGCAATAGTACGGTGGAGGCGCATCCAGGTATGATGATGGCAGCGCGAGTGGCG 180
QY 221 GAGCTGCTGCTGCTCCACGCGCGGAGCCCACTGCGCGCGGACCCCGCCACTCTCACCCGA 280
Db 181 GAGCTGCTGCTGCTCCACGCGCGGAGCCCACTGCGCGCGGACCCCGCCACTCTCACCCGA 240
QY 281 CCCGTGCACGACGCTGCCGCGGAGGCGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 340
Db 241 CCCGTGCACGACGCTGCCGCGGAGGCGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 300
QY 341 GGGCGCGGCTGGACGTGCGCGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 400
Db 301 GGGCGCGGCTGGACGTGCGCGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 360
QY 401 CTGGGCGCATGCGGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 460
Db 361 CTGGGCGCATGCGGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 420
QY 461 AACCATGCGCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATGGAAGAACAC 520
Db 421 AACCATGCGCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATGGAAGAACAC 480
QY 521 AGAGGCTCTGAGAAACCTCGGGGAGGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 580
Db 481 AGAGGCTCTGAGAAACCTCGGGGAGGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 540
QY 581 ACAACTGCCCCCGCCCAACCCACCGCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 640
Db 541 ACAACTGCCCCCGCCCAACCCACCGCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 600
QY 641 TTAATAATGCTGCTGCTTTTAAGCTAGATATAAGCCCTTCCCCACCTACCGTAAATGCCA 700
Db 601 TTAATAATGCTGCTGCTTTTAAGCTAGATATAAGCCCTTCCCCACCTACCGTAAATGCCA 660
QY 701 TTTATATCATTTTATATATCTTATATAATGTAAGCCCTTCCCCACCTACCGTAAATGCC 760
Db 661 TTTATATCATTTTATATATCTTATATAATGTAAGCCCTTCCCCACCTACCGTAAATGCC 720
QY 761 TTTTCACTGTTGGAGTTTCTGGAGTGAGCACTCACGCGCTTAAGCGCACATTCATGTG 820
Db 721 TTTTCACTGTTGGAGTTTCTGGAGTGAGCACTCACGCGCTTAAGCGCACATTCATGTG 780
QY 821 GGCATTTCTGGAGCCTCGCAGCCTCCGGAAGCTGTGCACTTCATGACAAGCATTTTGT 880
Db 781 GGCATTTCTGGAGCCTCGCAGCCTCCGGAAGCTGTGCACTTCATGACAAGCATTTTGT 840
QY 881 GAACTAGGAAAGCTCAGGCGGTTACTGCTCTCTTGTAGTACACTGCTAGCAATGSC 940
Db 841 GAACTAGGAAAGCTCAGGCGGTTACTGCTCTCTTGTAGTACACTGCTAGCAATGSC 900
QY 941 AGAACCAAGCTCAATATAAATAAATATTTTTCATTCATTCACCTC 987
Db 901 AGAACCAAGCTCAATATAAATAAATATTTTTCATTCATTCACCTC 947

RESULT 6
V53851
ID V53851 standard; cDNA; 947 BP.
AC V53851;
DT 04-DEC-1998 (first entry)
DE Coding sequence 3 of the multiple tumour suppressor 1.
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
PN U55801236-A.

PD 01-SEP-1998. 480810.
PF 07-JUN-1995; US-480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 98-494842/42.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Claim 1: Fig 17: 73bp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor 1
CC (MTS-1) gene, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

Query Match 94.9%; Score 943.8; DB 1; Length 947;
Best Local Similarity 99.8%; Pred. No. 4.1e-203;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 ATGGATCCGGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGCCACGCGCGG 100
Db 1 ATGGAGCGCGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGCCACGCGCGG 60
QY 101 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 160
Db 61 GCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGTGCGCTGCCCAACGCA 120
QY 161 CGCAATAGTACGGTGGAGGCGCATCCAGGTATGATGATGGCAGCGCGAGTGGCG 220
Db 121 CGCAATAGTACGGTGGAGGCGCATCCAGGTATGATGATGGCAGCGCGAGTGGCG 180
QY 221 GAGCTGCTGCTGCTCCACGCGCGGAGCCCACTGCGCGCGGACCCCGCCACTCTCACCCGA 280
Db 181 GAGCTGCTGCTGCTCCACGCGCGGAGCCCACTGCGCGCGGACCCCGCCACTCTCACCCGA 240
QY 281 CCCGTGCACGACGCTGCCGCGGAGGCGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 340
Db 241 CCCGTGCACGACGCTGCCGCGGAGGCGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 300
QY 341 GGGCGCGGCTGGACGTGCGCGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 400
Db 301 GGGCGCGGCTGGACGTGCGCGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 360
QY 401 CTGGGCGCATGCGGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 460
Db 361 CTGGGCGCATGCGGATGCTGGGCGCGCTCTGCCCGTGGACCTGGCTGAGGAG 420
QY 461 AACCATGCGCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATGGAAGAACAC 520
Db 421 AACCATGCGCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGGATGGAAGAACAC 480
QY 521 AGAGGCTCTGAGAAACCTCGGGGAGGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 580
Db 481 AGAGGCTCTGAGAAACCTCGGGGAGGCTTCCTGGACACGCTGGTGTGCTCACCGGGCC 540
QY 581 ACAACTGCCCCCGCCCAACCCACCGCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 640

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Db 541 ACAACTGCCCCGCCACACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 600
Qy 641 TTAATAATGTCTGCTTAAACGTAGATATAAGCCTTCCGCCACTACCGTAAATGTCCA 700
Db 601 TTAATAATGTCTGCTTAAACGTAGATATAAGCCTTCCGCCACTACCGTAAATGTCCA 660
Qy 701 TTTATATCATTTTTTATATATCTTATAAATGTAAAAATGTAAAAAGAAAAACACCGCTTCTGCC 760
Db 661 TTTATATCATTTTTTATATATCTTATAAATGTAAAAATGTAAAAAGAAAAACACCGCTTCTGCC 720
Qy 761 TTTTCACTGTGTGAGTTTCTCGAGTGCAGCTCAGCCCTAAGCGGCACATTCATGTG 820
Db 721 TTTTCACTGTGTGAGTTTCTCGAGTGCAGCTCAGCCCTAAGCGGCACATTCATGTG 780
Qy 821 GGCATTTCTCGAGCTCGCAGCTCGGAAGCTGTCGACTTCATGACAAAGCATTTTGT 880
Db 781 GGCATTTCTCGAGCTCGCAGCTCGGAAGCTGTCGACTTCATGACAAAGCATTTTGT 840
Qy 881 GAATAGGAAAGCTCAGGGGGTTACTGGCTTCTCTTGAGTGCACACTGCTAGCAAAATGGC 940
Db 841 GAATAGGAAAGCTCAGGGGGTTACTGGCTTCTCTTGAGTGCACACTGCTAGCAAAATGGC 900
Qy 941 AGAACCAAGCTCAATAAATAAATAAATTTTTCATTCATTCACCTC 987
Db 901 AGAACCAAGCTCAATAAATAAATAAATTTTTCATTCATTCACCTC 947

RESULT 7
V70615
ID V70615 standard; cDNA; 947 BP.
AC V70615;
DE 03-FEB-1999 (first entry)
KW cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.
OS Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
FH Homo sapiens.
FT Key
FT misc_feature 151
FT Location/Qualifiers
FT misc_feature 458 /tag= a
FT misc_feature 458 /note= "splice site acceptor"
FT misc_feature 458 /tag= b
FT misc_feature 458 /note= "splice site acceptor"
US5843756-A.
PN 01-DEC-1998.
PD 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
PT Mouse multiple tumour suppressor gene segment - useful for primer design
PS Disclosure; Fig 17; 80pp; English.
CC The present sequence represents the cDNA sequence for a human multiple tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

Query Match 94.9%; Score 943.8; DB 1; Length 947;
Best Local Similarity 99.8%; Pred. No. 4.1e-203;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 41 ATGATCGCGCGGGGAGCAGATGAGCCTTCGGCTGACTGCTGCGCAGCGCGCGCG 100
Db 1 ATGAGCGCGCGGGGAGCAGATGAGCCTTCGGCTGACTGCTGCGCAGCGCGCG 60
Qy 101 GCCCGGGTCTGGTAGAGAGGTGCGGCGCTGCTGGAGGCGGTGGCGCTGCCCAACGCA 160
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Db 61 GCCCGGGTCTGGTAGAGAGGTGCGGCGCTGCTGGAGCGGGGGCGCTGCCCAACGCA 120
Qy 161 CCGAATAGTTACGGTCCGAGGCCGATCCAGGTCATGATGATGGCGGCCGCCAGTGGCG 220
Db 121 CCGAATAGTTACGGTCCGAGGCCGATCCAGGTCATGATGATGGCGGCCGCCAGTGGCG 180
Qy 221 GAGCTGCTGTCTCACGCGCGGAGCCCACTGGCCGACCCCGCCACTCTCACCCGA 280
Db 181 GAGCTGCTGTCTCACGCGCGGAGCCCACTGGCCGACCCCGCCACTCTCACCCGA 240
Qy 281 CCCGTGCACGACCTCCCGGGAGGCTTCTCGACACGCTGTGTGTGTCACCGGCG 340
Db 241 CCCGTGCACGACCTCCCGGGAGGCTTCTCGACACGCTGTGTGTGTCACCGGCG 300
Qy 341 GGGCGCGGTGGACGTGGCGATGCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAG 400
Db 301 GGGCGCGGTGGACGTGGCGATGCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAG 360
Qy 401 CTGGCCATCGCATGTCGACGCTACCTGCGCGGGGCTGCGGGGGGCCACCAAGGAGT 460
Db 361 CTGGCCATCGCATGTCGACGCTACCTGCGCGGGGCTGCGGGGGGCCACCAAGGAGT 420
Qy 461 AACCATGCCCGCATAGATGCCGGAAGTCCCTCAGACATCCCGGATTCGAAAGAACCCAG 520
Db 421 AACCATGCCCGCATAGATGCCGGAAGTCCCTCAGACATCCCGGATTCGAAAGAACCCAG 480
Qy 521 AGAGGCTCTGAGAAACCTCGGAAACCTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 580
Db 481 AGAGGCTCTGAGAAACCTCGGAAACCTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 540
Qy 581 ACAACTGCCCCCGCCACACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 640
Db 541 ACAACTGCCCCCGCCACACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT 600
Qy 641 TTAATAATGTCTGCTTAAACGTAGATATAAGCCTTCCGCCACTACCGTAAATGTCCA 700
Db 601 TTAATAATGTCTGCTTAAACGTAGATATAAGCCTTCCGCCACTACCGTAAATGTCCA 660
Qy 701 TTTATATCATTTTTTATATATCTTATAAATGTAAAAATGTAAAAAGAAAAACACCGCTTCTGCC 760
Db 661 TTTATATCATTTTTTATATATCTTATAAATGTAAAAATGTAAAAAGAAAAACACCGCTTCTGCC 720
Qy 761 TTTTCACTGTGTGAGTTTCTGGAGTGCAGCTCAGCCCTAAGCGGCACATTCATGTG 820
Db 721 TTTTCACTGTGTGAGTTTCTGGAGTGCAGCTCAGCCCTAAGCGGCACATTCATGTG 780
Qy 821 GGCATTTCTTGGAGCTCGCAGCTCCGAGCCTCGGAAAGCTGTCGACTTCATGACAAAGCATTTGT 880
Db 781 GGCATTTCTTGGAGCTCGCAGCTCCGAGCCTCGGAAAGCTGTCGACTTCATGACAAAGCATTTGT 840
Qy 881 GAATAGGAAAGCTCAGGGGGTTACTGGCTTCTCTTGAGTGCACACTGCTAGCAAAATGGC 940
Db 841 GAATAGGAAAGCTCAGGGGGTTACTGGCTTCTCTTGAGTGCACACTGCTAGCAAAATGGC 900
Qy 941 AGAACCAAGCTCAATAAATAAATAAATTTTTCATTCATTCACCTC 987
Db 901 AGAACCAAGCTCAATAAATAAATAAATTTTTCATTCATTCACCTC 947

RESULT 8
Q63491
ID Q63491 standard; DNA; 948 BP.
AC Q63491;
DE 07-DEC-1994 (first entry)
KW Inhibitor of cyclin dependent kinase 4 (p16INK4).
KW Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;
KW lymphoma; cell cycle; detection; identification; tumour virus;
OS Proliferating cell nuclear antigen; subunit; complex; ss; ds.
FH Homo sapiens.
FT Key
FT Location/Qualifiers
FT misc_feature 19..465 /tag= a
FT misc_feature 19..465 /product= 16 kilodalton protein.
FT FT
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PN WO9409135-A.
PD 28-APR-1994.
PF 18-OCT-1993; U09945.
PR 16-OCT-1992; US-963308.
PA 17-DEC-1992; US-991997.
PI (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Xiong Y;
DR WPI: 94-151320/18.
DR P-PSDB; R53401.
PT Detection of subunit components of cyclin complexes - used for
PT diagnosing transformation of a cell and developing inhibitors and
PT activators, partic for cancer treatment
PS Claim 15; Page 39-40; 45pp; English.
CC The cell cycle gene implicated most strongly in oncogenesis is the
CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a
CC locus activated by translocation to an immunoglobulin gene enhancer
CC in some B-cell lymphomas and leukaemias. D-type cyclin, cyclin
CC dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and
CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many
CC combinatorial variations of the components e.g. cyclin D1 or D3 and
CC Cdk2, Cdk4 and Cdk5, assemble in vivo. Each quaternary complex may
CC have a subtly different role in the cell cycle or in different cell
CC types. Cellular transformation by DNA tumour viruses such as SV40
CC is associated with selective subunit rearrangement of the cyclin D
CC complexes. In virally transformed cells, Cdk4 totally dissociates
CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton
CC polypeptide (p16). This nucleotide sequence encodes a 16 kDa
CC protein, designated p16INK4 which binds to and inhibits Cdk4. This
CC polypeptide was discovered to show many similarities to p16.
CC Reagents, such as monoclonal antibodies, can be developed that
CC recognise the interactions between the Cdk's cyclins, PCNA and low
CC molecular weight polypeptides and can therefore be used to identify
CC the state of transformation of a cell.
SQ Sequence 948 BP; 215 A; 270 C; 266 G; 197 T;

Query Match 94.3%; Score 937.6; DB 1; Length 948;
Best Local Similarity 99.6%; Pred. No. 1e-201; Mismatches 0; Gaps 0;
Matches 940; Conservative 0; Indels 4;

QY 51 CGCGCGGAGCAGCATGGAGCCCTTCGGCTGACGTGGCTGGCCAGCGCGCGCGCGGGT 110
DB 5 CGCGCAGGAGCAGCATGGAGCCCTTCGGCTGACGTGGCTGGCCAGCGCGCGCGGGT 64
QY 111 GGGTAGAGGAGTCCGGCGCTCTCTGGAGCGGTGGCGTGGCCAGCGCGCGCGAGT 170
DB 65 GGGTAGAGGAGTCCGGCGCTCTCTGGAGCGGTGGCGTGGCCAGCGCGCGAGT 124
QY 171 ACGGTGGAGCGCGATCCAGGTCTCTGGAGCGGTGGCGTGGCCAGCGCGCGAGT 230
DB 125 ACGGTGGAGCGCGATCCAGGTCTCTGGAGCGGTGGCGTGGCCAGCGCGAGT 184
QY 231 TGGTCCAGCGCGCGAGCGCGCACTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 290
DB 185 TGGTCCAGCGCGCGAGCGCGCACTGGCGCGCGCGCGCGCGCGCGCGCGCG 244
QY 291 ACGGTGGCGCGCGAGCGGTCTCTGGAGCGGTGGCGTGGCCAGCGCGCGAGT 350
DB 245 ACGGTGGCGCGCGAGCGGTCTCTGGAGCGGTGGCGTGGCCAGCGCGCGAGT 304
QY 351 TGGAGTGGCGCGATGGCTGGCGCGCGGTCTGGCGCGCGGTGGCGCGCGCGCG 410
DB 305 TGGAGTGGCGCGATGGCTGGCGCGCGGTCTGGCGCGCGGTGGCGCGCGCGCG 364
QY 411 GCGATGTCGCGACGCGTCTCTGGCGCGCGGTCTGGCGCGCGGTGGCGCGCGCG 470
DB 365 GCGATGTCGCGACGCGTCTCTGGCGCGCGGTCTGGCGCGCGGTGGCGCGCG 424
QY 471 GCATAGTCCCGGAGAGTCCCTTCAGACATCCCGCGATCCCGCGATCCCGCGAT 530
DB 425 GCATAGTCCCGGAGAGTCCCTTCAGACATCCCGCGATCCCGCGATCCCGCGAT 484
QY 531 AGAACCCTCGGGAACCTTAGATCATCATAGTCACCGAGGTCTCTACAGGGCCACAGTCC 590

DB 485 AGAACCCTCGGGAACCTTAGATCATCATAGTCACCGAGGTCTCTACAGGGCCACAGTCC 544
QY 591 CGGCCACACACCACCCCGCTTCGTTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGT 650
DB 545 CGGCCACACACCACCCCGCTTCGTTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGT 604
QY 651 CTTGCGCTTTTAAAGCTAGATATAGCTTCCCGCAGTACCGTAAATGCTCCATTATATCAT 710
DB 605 CTTGCGCTTTTAAAGCTAGATATAGCTTCCCGCAGTACCGTAAATGCTCCATTATATCAT 664
QY 711 TTTTATATATTTCTTATAAAATGTAAGAAAGAAAACACCGCTTCGCTCTTTTCACTGT 770
DB 665 TTTTATATATTTCTTATAAAATGTAAGAAAGAAAACACCGCTTCGCTCTTTTCACTGT 724
QY 771 GTTGGAGTTTTCTGGAGTGAGCAGTACACGCCCTTAAGCGCAGCATTCATGTGGCACTTTCT 830
DB 725 GTTGGAGTTTTCTGGAGTGAGCAGTACACGCCCTTAAGCGCAGCATTCATGTGGCACTTTCT 784
QY 831 GCGAGCTCGCAGCGCTCCGGAAGCTGTGCACATTCATGACAAGCATTTTGTGAAGTAGGA 890
DB 785 GCGAGCTCGCAGCGCTCCGGAAGCTGTGCACATTCATGACAAGCATTTTGTGAAGTAGGA 844
QY 891 AGCTCAGGGGGTGTACTGGCTTCTCTTGTAGTCACACTGTAGCAAAATGCGAAGCAAAAG 950
DB 845 AGCTCAGGGGGTGTACTGGCTTCTCTTGTAGTCACACTGTAGCAAAATGCGAAGCAAAAG 904
QY 951 CTCATAATAAAATAAAATTTATTTTTCATTCATTCACCTCAAAAAA 994
DB 905 CTCATAATAAAATAAAATTTATTTTTCATTCATTCACCTCAAAAAA 948

RESULT 9
T00744 ID T00744 standard; cDNA; 1131 BP.
AC T00744;
DT 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) gene ORF.
KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;
KW Predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 338..655 /*tag= a
PN WO9525813-Al.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI: 95-344626/44.
DR P-PSDB; R81700.
PT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Example 7; Pages 100-101; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the
CC MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay
CC can also be used in the diagnosis and prognosis of melanoma,
CC lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 80.6%; Score 801; DB 1; Length 1131;
Best Local Similarity 100.0%; Pred. No. 4.7e-171;


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Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 CCAGGTATGATGGCGAGCCCGAGTGGCGAGGCTGCTGCTCCACGGCGCGGA 246
DB 331 CCAGGTATGATGGCGAGCCCGAGTGGCGAGGCTGCTGCTCCACGGCGCGGA 390
QY 247 GCCCAACTGGCGGACCCCGCCTCTCACCGGACCCGTGACAGAGCTGCGCGGAGGG 306
DB 391 GCCCAACTGGCGGACCCCGCCTCTCACCGGACCCGTGACAGAGCTGCGCGGAGGG 450
QY 307 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 366
DB 451 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 510
QY 367 CTGGGCGGCTGTCGCGGACCTGGCTGAGAGCTGGGCCATCGCGATGTCGACGGTA 426
DB 511 CTGGGCGGCTGTCGCGGACCTGGCTGAGAGCTGGGCCATCGCGATGTCGACGGTA 570
QY 427 CTGGGCGGCTGTCGCGGACCCAGAGGCACTGAGAGCTGGGCCATCGCGATGTCGACGGTA 486
DB 571 CTGGGCGGCTGTCGCGGACCCAGAGGCACTGAGAGCTGGGCCATCGCGATGTCGACGGTA 570
QY 307 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 366
DB 451 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 510
QY 367 CTGGGCGGCTGTCGCGGACCTGGCTGAGAGCTGGGCCATCGCGATGTCGACGGTA 426
DB 511 CTGGGCGGCTGTCGCGGACCCAGAGGCACTGAGAGCTGGGCCATCGCGATGTCGACGGTA 570
QY 427 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 366
DB 571 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 570
QY 367 CTGGGCGGCTGTCGCGGACCTGGCTGAGAGCTGGGCCATCGCGATGTCGACGGTA 426
DB 511 CTGGGCGGCTGTCGCGGACCCAGAGGCACTGAGAGCTGGGCCATCGCGATGTCGACGGTA 570
QY 427 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 366
DB 571 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 570
QY 487 AGGTCCCTCAGACATCCCGGATGAAAGAACCCAGAGAGGCTCTGAGAAACCTCGGGAAC 546
DB 631 AGGTCCCTCAGACATCCCGGATGAAAGAACCCAGAGAGGCTCTGAGAAACCTCGGGAAC 590
QY 547 TTAGATCATCAGTACCGAAGGCTCTACAGGGCCACAACTGCCCCCGCACAAACCCACC 606
DB 691 TTAGATCATCAGTACCGAAGGCTCTACAGGGCCACAACTGCCCCCGCACAAACCCACC 750
QY 607 CGCTTTCTGAGTTTCATTTAGAAAATAGAGCTTTTAAATAGCTGCTGCTTTTAAAGCTA 666
DB 751 CGCTTTCTGAGTTTCATTTAGAAAATAGAGCTTTTAAATAGCTGCTGCTTTTAAAGCTA 810
QY 667 GATATAAGCTTCCCGCCACTACCGTAATGTCCATTTATATATATATATATATATCTTA 726
DB 811 GATATAAGCTTCCCGCCACTACCGTAATGTCCATTTATATATATATATATATCTTA 870
QY 727 TAAATGTTAAAGAAAGAAAAACACCGCTTCTGCGCTTTTCACTGTTGAGTTTCTGGA 786
DB 871 TAAATGTTAAAGAAAGAAAAACACCGCTTCTGCGCTTTTCACTGTTGAGTTTCTGGA 930
QY 787 GTGAGACTCAGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTCGAGGCTTCGAGCCT 846
DB 931 GTGAGACTCAGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTCGAGGCTTCGAGCCT 990
QY 847 CCGGAGCTGTCGACTCATGACAGCATTTTGTGAAGTGGGAGCTCAGGGGGTTAC 906
DB 991 CCGGAGCTGTCGACTCATGACAGCATTTTGTGAAGTGGGAGCTCAGGGGGTTAC 1050
QY 907 TGGCTTCTCTTTCAGTACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAAAATAA 966
DB 1051 TGGCTTCTCTTTCAGTACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAAAATAA 1110
QY 967 ATTATTTTCATTTCACTC 987
DB 1111 ATTATTTTCATTTCACTC 1131
RESULT 10
Q99164
ID Q99164 standard; cdna; 1131 BP.
AC Q99164;
DT 03-MAY-1996 (first entry)
DE Human MTS polypeptide, MTS1E1-beta encoding cdna.
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW gene therapy; chronic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 338..655
FT /*tag= a
FT /*product= MTS1E1-beta
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PN W09525429-AL.
PD 28-SEP-1995.
PF 17-MAR-1995; U03316.
PR 18-MAR-1994; US-214581.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215088.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 95-344401/44.
DR P-PSDB; R80947.
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
PS Claim 4; Page 100-101; 156pp; English.
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC polypeptides have been isolated and sequenced. This sequence encodes
CC the MTS polypeptide MTS1E1-beta (R80947). MTS polypeptide-encoding cDNAs
CC and mutants of these are useful for the diagnosis or prognosis of
CC human cancer. Germ-line mutations of MTS cDNAs can be used for
CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,
CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers
CC of the pancreas, thyroid, ovary, uterus, kidney, stomach and
CC rectum. The wild-type gene is useful for gene therapy and MTS
CC polypeptides may also be used for protein replacement therapy. Also
CC the polypeptides or cells contg. an altered MTS gene are useful for
CC screening for potential cancer therapeutics.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
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Query Match 80.6%; Score 801; DB 1; Length 1131;
Best Local Similarity 100.0%; Pred. No. 4.7e-171;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 187 CCAGGTATGATGGCGAGCCCGAGTGGCGAGGCTGCTGCTCCACGGCGCGGA 246
DB 331 CCAGGTATGATGGCGAGCCCGAGTGGCGAGGCTGCTGCTCCACGGCGCGGA 390
QY 247 GCCCAACTGGCGGACCCCGCCTCTCACCGGACCCGTGACAGAGCTGCGCGGAGGG 306
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QY 307 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 366
DB 451 CTTCTGGACAGCTGGTGGTCTGACCGGCGGGCGGCGGCTGGAGTGGCGGATGC 510
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DB 631 AGGTCCCTCAGACATCCCGGATGAAAGAACCCAGAGAGGCTCTGAGAAACCTCGGGAAC 590
QY 547 TTAGATCATCAGTACCGAAGGCTCTACAGGGCCACAACTGCCCCCGCACAAACCCACC 606
DB 691 TTAGATCATCAGTACCGAAGGCTCTACAGGGCCACAACTGCCCCCGCACAAACCCACC 750
QY 607 CGCTTTCTGAGTTTCATTTAGAAAATAGAGCTTTTAAATAGCTGCTGCTTTTAAAGCTA 666
DB 751 CGCTTTCTGAGTTTCATTTAGAAAATAGAGCTTTTAAATAGCTGCTGCTTTTAAAGCTA 810
QY 667 GATATAAGCTTCCCGCCACTACCGTAATGTCCATTTATATATATATATATATCTTA 726
DB 811 GATATAAGCTTCCCGCCACTACCGTAATGTCCATTTATATATATATATATCTTA 870
```


PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PS Claim 1; Fig 12; 72pp; English.

CC This cDNA sequence encodes a human multiple tumour suppressor protein,
CC MTS1E1-beta. The MTS gene locus is also referred to as the familial
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

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Query Match      80.6%; Score 801; DB 1; Length 1131;
Best Local Similarity 100.0%; Pred. No. 4.7e-171;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CCAGGTGATGATGGGCGAGCGCGGAGTGGCGGAGTCTGCTGCTCCACGGCGCGGA 246
    |||
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QY 247 GCCCAACTGCGCGACCGCGGACCTCTCACCCGACCGGTGCGACGCTGCCGGGAGG 306
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Db 391 GCCCAACTGCGCGACCGCGGACCTCTCACCCGACCGGTGCGACGCTGCCGGGAGG 450
    |||
QY 307 CTTCCTGGACACGCTGGTGGTGTGACCGGGCGGGGGCGGCTGGAGTGGCGGATGC 366
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QY 487 AGGTCCCTAGACATCCCGGATGAAAGAACACAGAGAGGTCTTGAGAACTCGGGAAC 546
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Db 631 AGGTCCCTAGACATCCCGGATGAAAGAACACAGAGAGGTCTTGAGAACTCGGGAAC 690
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QY 547 TTAGATCATGTCACCGAGGTCTTACAGGGCCACACTGCCCGCCGACACCCACCC 606
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Db 691 TTAGATCATGTCACCGAGGTCTTACAGGGCCACACTGCCCGCCGACACCCACCC 750
    |||
QY 607 CGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAATAATGCTCTTTAAAGTA 666
    |||
Db 751 CGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAATAATGCTCTTTAAAGTA 810
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QY 667 GATATAAGCCTTCCCGCACTACCGTAAATGTCCATTTATATCATTTTATATTTCTTA 726
    |||
Db 811 GATATAAGCCTTCCCGCACTACCGTAAATGTCCATTTATATCATTTTATATTTCTTA 870
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QY 727 TAAATGTAATAAGAAAACACCGCTTCTGCGCTTTTCTACTGTTGGAGTTTCTTGA 786
    |||
Db 871 TAAATGTAATAAGAAAACACCGCTTCTGCGCTTTTCTACTGTTGGAGTTTCTTGA 930
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QY 787 GTGAGCACTACCGCCCTAAGCGCACATTCATGTGGGATTTCTTTCGAGGCTTCGACGCT 846
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Db 931 GTGAGCACTACCGCCCTAAGCGCACATTCATGTGGGATTTCTTTCGAGGCTTCGACGCT 990
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QY 847 CCGGAAGCTGTCGACTTCATGACAAAGCATTTTGTGAAGTGGAGAGTTCAGGGGGTTAC 906
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QY 907 TGGCTTCTTGTGATGACACTGTAGCAATATGGCAGAACCAAGCTCAATATAAATAA 966
    |||
Db 1051 TGGCTTCTTGTGATGACACTGTAGCAATATGGCAGAACCAAGCTCAATATAAATAA 1110
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QY 967 ATTATTTTCATTTCACTC 987
    |||
Db 1111 ATTATTTTCATTTCACTC 1131
    |||
```

RESULT 13
V53830

ID V53830 standard; cDNA; 1131 BP.

AC V53830;

DT 04-DEC-1998 (first entry)

DE Coding sequence 1 of the multiple tumour suppressor MTS1E1S.

KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 338..655

FT /product= "human MTS1E1S"

FT /tag= a

US5801236-A.

01-SEP-1998.

07-JUN-1995; 480810.

07-JUN-1995; US-480810.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-251938.

17-MAR-1995; WO-003316.

(MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-494842/42.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -

PT useful as hybridisation probes, primers and recombinant production

PT of MTS in the diagnosis and treatment of cancers related to MTS

PT mutation(s)

PS Example 7; Column 73-76; 73pp; English.

CC This is the nucleotide sequence of the multiple tumour suppressor

CC (MTS1E1S) gene, used in the method of the invention. The MTS gene

CC is useful in the diagnosis and prognosis of human cancer, e.g. by

CC standard nucleic hybridisation techniques, of patient samples. The

CC mutated sequences are those that are present in somatic mutations

CC of the gene in cancers. The vectors can be used for gene therapy

CC strategies to replace function of mutated protein in patients. These

CC can also be used to construct protein mimetics, also for therapeutic

CC strategies. In addition the expression constructs can also be used

CC for recombinant production of MTS. Recombinant MTS can be used to

CC screen for drugs to be used for cancer therapy, and the protein

CC itself may also be used to restore MTS function in a cell.

Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

SQ

Query Match 80.6%; Score 801; DB 1; Length 1131;

Best Local Similarity 100.0%; Pred. No. 4.7e-171;

Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 187 CCAGGTGATGATGGGCGAGCGCGGAGTGGCGGAGTCTGCTGCTCCACGGCGCGGA 246
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Db 331 CCAGGTGATGATGGGCGAGCGCGGAGTGGCGGAGTCTGCTGCTCCACGGCGCGGA 390
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QY 247 GCCCAACTGCGCGACCGCGGACCTCTCACCCGACCGGTGCGACGCTGCCGGGAGG 306
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Db 391 GCCCAACTGCGCGACCGCGGACCTCTCACCCGACCGGTGCGACGCTGCCGGGAGG 450
    |||
QY 307 CTTCCTGGACACGCTGGTGGTGTGACCGGGCGGGGGCGGCTGGAGTGGCGGATGC 366
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QY 427 CCTGCGCGGTCTGGGGGGGACCGAGTGGCGGAGTCTGCTGCTCCACGGCGCGGA 486
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Db 571 CCTGCGCGGTCTGGGGGGGACCGAGTGGCGGAGTCTGCTGCTCCACGGCGCGGA 630
    |||
QY 487 AGGTCCCTAGACATCCCGGATGAAAGAACACAGAGAGGTCTTGAGAACTCGGGAAC 546
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Db 631 AGTCTCCTCAGACATCCCGGATTGAAGAAACAGAGAGGCTCTGAGAAACCTCGGGAAC 690
QY 547 TTAGATCATCAGTACCGAAGTCTTACAGGGCCACAACTGCCCGGCCACAAACCCACCC 606
Db 691 TTAGATCATCAGTACCGAAGTCTTACAGGGCCACAACTGCCCGGCCACAAACCCACCC 750
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QY 667 GATATAAGCTTCCCGCCACTACCGTAAATGTCATTTATATATATATATATATATATAT 726
Db 811 GATATAAGCTTCCCGCCACTACCGTAAATGTCATTTATATATATATATATATATAT 870
QY 727 TAAAAATGTAAAAAGAAAACACCCGCTTCTGCTCTTTTCACTGTGTGGAGTTTCTGGA 786
Db 871 TAAAAATGTAAAAAGAAAACACCCGCTTCTGCTCTTTTCACTGTGTGGAGTTTCTGGA 930
QY 787 GTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGGCATTTCTTGGAGCTCGCAGCCT 846
Db 931 GTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGGCATTTCTTGGAGCTCGCAGCCT 990
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QY 907 TGGCTTCTTGTAGTACACTGTAGCAATATGCGAAGCAAGCTCAATATAAAATAAA 966
Db 1051 TGGCTTCTTGTAGTACACTGTAGCAATATGCGAAGCAAGCTCAATATAAAATAAA 1110
QY 967 ATTATTTTCATTCATTCACCTC 987
Db 1111 ATTATTTTCATTCATTCACCTC 1131

RESULT 14

V70594
ID V70594 standard; cDNA: 1131 BP.
AC V70594;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a human multiple tumour suppressor 1E1-beta protein.
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 338..655
FT /tag= a
FT /product= MTS1E1-beta
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
DR P-PSDB; W80525.
PT Mouse multiple tumour suppressor gene segment - useful for primer design
PS Example 8: Fig 12A-B; 80pp; English.
CC The present sequence encodes a human multiple tumour suppressor 1E1-beta
CC (MTS1E1-beta) protein. Primers designed from the gene can be used to
CC design primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 1131 BP; 231 A; 327 C; 344 G; 229 T;
Query Match 80.6%; Score 801; DB 1; Length 1131;
Best Local Similarity 100.0%; Pred. No. 4.7e-171;
Matches 801; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 187 CCAGGTCATGATGAGGCGAGCGCCCGAGTGGCGGAGCTCTGCTGCCACGCGCGGA 246

Db 331 CCAGGTCATGATGGGAGCGCCGAGTGGCGAGCTGCTGCTCTCCACGCGCGGA 390
QY 247 GCCCAACTGGCGGACCCCGCCACTCTCACCGACCCGCTGCAGAGCTGCGCGGGAGGG 306
Db 391 GCCCAACTGGCGGACCCCGCCACTCTCACCGACCCGCTGCAGAGCTGCGCGGGAGGG 450
QY 307 CTTCTCGACAGCTGGTGGTGTGCACCGGGCGGGGGCGGCTGGAGCTGGCGGATGC 366
Db 451 CTTCTCGACAGCTGGTGGTGTGCACCGGGCGGGGGCGGCTGGAGCTGGCGGATGC 510
QY 367 CTGGGGCGCTGCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGGATGTCGACGGTA 426
Db 511 CTGGGGCGCTGCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCGGATGTCGACGGTA 570
QY 427 CTTGCGCGGGGCTGCGGGGGGACACAGAGCAGTAACCATGCCGCATAGATGCCCGGA 486
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QY 487 AGTCCCTCAGACATCCCGGATTGAAAGAACAGAGAGGCTCTGAGAAAGCTCGGGAAC 546
Db 631 AGTCCCTCAGACATCCCGGATTGAAAGAACAGAGAGGCTCTGAGAAAGCTCGGGAAC 690
QY 547 TTAGATCATCAGTCACCGAAGTCTTACAGGGCCACAACTGCCCGCCACAAACCCACCC 606
Db 691 TTAGATCATCAGTCACCGAAGTCTTACAGGGCCACAACTGCCCGCCACAAACCCACCC 750
QY 607 CGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTGCTTTTAACGTA 666
Db 751 CGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTGCTTTTAACGTA 810
QY 667 GATATAAGCTTCCCGCCACTACCGTAAATGTCCATTTATATATATATATATATAT 726
Db 811 GATATAAGCTTCCCGCCACTACCGTAAATGTCCATTTATATATATATATATATAT 870
QY 727 TAAAAATGTAAAAAGAAAACACCCGCTTCTGCTCTTTTCACTGTGTGGAGTTTCTGGA 786
Db 871 TAAAAATGTAAAAAGAAAACACCCGCTTCTGCTCTTTTCACTGTGTGGAGTTTCTGGA 930
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Db 931 GTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGGCATTTCTTGGAGCTCGCAGCCT 990
QY 847 CGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGCTCAGGGGGTTAC 906
Db 991 CGGAAGCTGTGACATTCATGACAAGCATTTTGTGAAGTGGGAGCTCAGGGGGTTAC 1050
QY 907 TGGCTTCTTGTAGTACACTGTAGCAATATGCGAAGCAAGCTCAATATAAAATAAA 966
Db 1051 TGGCTTCTTGTAGTACACTGTAGCAATATGCGAAGCAAGCTCAATATAAAATAAA 1110
QY 967 ATTATTTTCATTCATTCACCTC 987
Db 1111 ATTATTTTCATTCATTCACCTC 1131

RESULT 15

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ID T74051 standard; cDNA: 1420 BP.
AC T74051;
DT 16-MAR-1998 (first entry)
DE CDK inhibitory fusion protein coding sequence #1.
KW Fusion gene; CDK inhibitor; cyclin-dependent kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 4..1179
FT /tag= a
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GenCore version 4.5
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Title: US-09-016-869A-1

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SUMMARIES

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7	943.8	94.9	947	2	US-08-487-033-36
8	943.8	94.9	947	2	US-08-480-810-36
9	943.8	94.9	947	3	US-08-508-733-36
10	943.8	94.9	947	4	US-08-848-251-36
11	943.8	94.9	947	4	US-08-486-047-36
12	943.8	94.9	947	5	US-09-120-130-36
13	943.8	94.9	947	5	US-09-115-252-36
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ALIGNMENTS

RESULT 1
US-08-627-610-1
; Sequence 1, Application US/08627610
; Patent No. 591997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Definho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 41..508
US-08-627-610-1

Query Match 100.0%; Score 994; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 4.9e-225;

Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGCAGCATGATCCGGCGGGGGAG	60						
Db	1	CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGCAGCATGATCCGGCGGGGGAG	60						
Qy	61	CAGCATGGAGCCTTCGGCTGACTGGCTGGCCACCGCCGCGGGTGGGTAGAGGA	120						
Db	61	CAGCATGGAGCCTTCGGCTGACTGGCTGGCCACCGCCGCGGGTGGGTAGAGGA	120						
Qy	121	GTCGGGCGCTGCTGGAGGGGTGGCGCTGCCAACGACCCAGTATAGTACGGTCGGAG	180						
Db	121	GTCGGGCGCTGCTGGAGGGGTGGCGCTGCCAACGACCCAGTATAGTACGGTCGGAG	180						
Qy	181	GCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGTCTCCACGG	240						
Db	181	GCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGTCTCCACGG	240						
Qy	241	CGCGAGCCCAACTGCGCCGACCCGCACTCTCACCGGACCCGTCGACGACGTCGCCG	300						
Db	241	CGCGAGCCCAACTGCGCCGACCCGCACTCTCACCGGACCCGTCGACGACGTCGCCG	300						
Qy	301	GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG	360						
Db	301	GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG	360						
Qy	361	CGATGCTGGGGCGCTGTCGCGGTGGACCTGGCTGGAGAGTGGGCCATCGCATGTCG	420						
Db	361	CGATGCTGGGGCGCTGTCGCGGTGGACCTGGCTGGAGAGTGGGCCATCGCATGTCG	420						
Qy	421	ACGCTACTGCGCGGCTGCGGGGGGACCCAGAGGAGTAAACATGCCCGCATAGATGC	480						
Db	421	ACGCTACTGCGCGGCTGCGGGGGGACCCAGAGGAGTAAACATGCCCGCATAGATGC	480						
Qy	481	CGCGGAAGGTCCCTCAGACATCCCGGATGAAAGAACAGAGAGGCTCTGAGAAACCTCG	540						
Db	481	CGCGGAAGGTCCCTCAGACATCCCGGATGAAAGAACAGAGAGGCTCTGAGAAACCTCG	540						
Qy	541	GGAACCTAGATCATGATCAGTACCAAGGTCTACAGGCCACACTGCCCGCCCAAC	600						
Db	541	GGAACCTAGATCATGATCAGTACCAAGGTCTACAGGCCACACTGCCCGCCCAAC	600						
Qy	601	CCACCCGCTTTCGTAGTTTTCATTTAGAAATAGCTTTTAAATGCTCTGCTCTTT	660						
Db	601	CCACCCGCTTTCGTAGTTTTCATTTAGAAATAGCTTTTAAATGCTCTGCTCTTT	660						
Qy	661	AACGTAGATATAAGCCTTCCCGCACTACCGTAAATGTCCATTTATATCAATTTTATA	720						
Db	661	AACGTAGATATAAGCCTTCCCGCACTACCGTAAATGTCCATTTATATCAATTTTATA	720						
Qy	721	TCTTTTAAATGTAAAAAGAAAAACACCGCTTCTGCTTTTCACTGTGTTGAGTTT	780						
Db	721	TCTTTTAAATGTAAAAAGAAAAACACCGCTTCTGCTTTTCACTGTGTTGAGTTT	780						
Qy	781	TCTGAGTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGCATTTCTTCCGAGCCTCG	840						
Db	781	TCTGAGTGAGCACTCAGCCCTTAAGCGCACATTCATGTGGCATTTCTTCCGAGCCTCG	840						
Qy	841	CAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCAATTTGTGAAGTGGAGCTCAGGGG	900						
Db	841	CAGCCTCCGGAAGCTGTCGACTTCATGACAAAGCAATTTGTGAAGTGGAGCTCAGGGG	900						
Qy	901	GTTTACTGGCTTCTTGTGAGTCACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA	960						
Db	901	GTTTACTGGCTTCTTGTGAGTCACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA	960						
Qy	961	AATAAATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	994						
Db	961	AATAAATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC	994						

Sequence 1, Application US/08306511A
Patent No. 5962316
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 41..508
US-08-306-511A-1

Query Match 100.0%; Score 994; DB 4; Length 994;
Best Local Similarity 100.0%; Pred. No. 4.9e-225;
Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGCAGCATGATCCGGCGGGGGAG	60
Db	1	CGGAGAGGGGAGAACAGAACACGGGGGGGGGAGCAGCATGATCCGGCGGGGGAG	60
Qy	61	CAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGGTGGGTAGAGGA	120
Db	61	CAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGGTGGGTAGAGGA	120
Qy	121	GTCGGGCGCTGCTGGAGCGGTGGCGCTGCCAACGACCCAGTATAGTACGGTCGGAG	180
Db	121	GTCGGGCGCTGCTGGAGCGGTGGCGCTGCCAACGACCCAGTATAGTACGGTCGGAG	180
Qy	181	GCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGTCTCCACGG	240
Db	181	GCCGATCCAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGTCTCCACGG	240
Qy	241	CGCGAGCCCAACTGCGCCGACCCGCACTCTCACCGGACCCGTCGACGACGTCGCCG	300
Db	241	CGCGAGCCCAACTGCGCCGACCCGCACTCTCACCGGACCCGTCGACGACGTCGCCG	300
Qy	301	GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG	360
Db	301	GGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGG	360

541 GGAACCTAGATCATCAGTCACCGAAGGTCCTACAGGGGCACAACTGCCCGCCACAAAC 600
|||||
541 GGAACCTAGATCATCAGTCACCGAAGGTCCTACAGGGGCACAACTGCCCGCCACAAAC 600
601 CAACCCCGCTTCGTAAGTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTT 660
|||||
601 CAACCCCGCTTCGTAAGTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTT 660
661 AACGTAGATATAAGCCTTCCCCACCTACCGTAATGTCATTTATATATATATATATA 720
|||||
661 AACGTAGATATAAGCCTTCCCCACCTACCGTAATGTCATTTATATATATATATATA 720
721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTT 780
|||||
721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTT 780
781 TCTGGAGTGAGCACTCACGCCCTTAAGCGACATTCATGTGGGCAATTCCTGCGAGCCTCG 840
|||||
781 TCTGGAGTGAGCACTCACGCCCTTAAGCGACATTCATGTGGGCAATTCCTGCGAGCCTCG 840
841 CAGCCTCCGGAAGCTGCGACTTCATGACAAGCATTTTGTGAAGTGGGAAGCTCAGGGG 900
|||||
841 CAGCCTCCGGAAGCTGCGACTTCATGACAAGCATTTTGTGAAGTGGGAAGCTCAGGGG 900
901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960
|||||
901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960
961 AATAAAATATTATTTCACTTCACTCAAAAAA 994
|||||
961 AATAAAATATTATTTCACTTCACTCAAAAAA 994
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RESULT 5

PCT-US95-04636-1
; Sequence 1, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..508

PCT-US95-04636-1

Query Match 100.0%; Score 994; DB 6; Length 994;
Best Local Similarity 100.0%; Pred. No. 4.9e-225;
Matches 994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGAGAGGGGAGACAGACAGCGCGCGGGGAGCAGCATGGATCCGGCGCGGGAG 60
|||||
DB 1 CGGAGAGGGGAGACAGACAGCGCGCGGGGAGCAGCATGGATCCGGCGCGGGAG 60
61 CAGCATGGAGCCTTCGGCTGACTGGCTGCCAGCGCGCGGGGCTGGGTAGAGGA 120
|||||
DB 61 CAGCATGGAGCCTTCGGCTGACTGGCTGCCAGCGCGCGGGGCTGGGTAGAGGA 120
QY 121 GGTGCGGCGCTGCTGGAGGCGGTGCGCTGCCCAACGACCGCAATAGTTACGGTCCGAG 180
|||||
DB 121 GGTGCGGCGCTGCTGGAGGCGGTGCGCTGCCCAACGACCGCAATAGTTACGGTCCGAG 180
QY 181 GCCGATCCAGGTCATGATGATGGGAGCGCCGAGTGGGAGCTGCTGCTGCCACGG 240
|||||
DB 181 GCCGATCCAGGTCATGATGATGGGAGCGCCGAGTGGGAGCTGCTGCTGCCACGG 240
QY 241 CGCGGAGCCCAACTGCGCGGACCCCGCCACTCTCACCCGACCGCTGCACGACGCTGCCG 300
|||||
DB 241 CGCGGAGCCCAACTGCGCGGACCCCGCCACTCTCACCCGACCGCTGCACGACGCTGCCG 300
QY 301 GGAGGCTTCCTGGACACGCTGCTGCTGCACCGCGCGGGCGCGGCTGGACGCTGG 360
|||||
DB 301 GGAGGCTTCCTGGACACGCTGCTGCTGCACCGCGCGGGCGCGGCTGGACGCTGG 360
QY 361 CGATGCTGGGCGCTGCTGCCGCTGAGGAGCTGGGCGCATCGCGATGCTGC 420
|||||
DB 361 CGATGCTGGGCGCTGCTGCCGCTGAGGAGCTGGGCGCATCGCGATGCTGC 420
QY 421 ACGGTACCTGCGCGGCTGCGGGGACACGAGGCGCTAACCATGCCGCATAGATGC 480
|||||
DB 421 ACGGTACCTGCGCGGCTGCGGGGACACGAGGCGCTAACCATGCCGCATAGATGC 480
QY 481 CGCGGAAGTTCCTCAGACATCCCGATTGAAGAACACGAGAGGCTCTGAGAACTCG 540
|||||
DB 481 CGCGGAAGTTCCTCAGACATCCCGATTGAAGAACACGAGAGGCTCTGAGAACTCG 540
QY 541 GGAACCTAGATCATCAGTCACCGAAGGTCCTACAGGGGCACAACTGCCCGCCACAAAC 600
|||||
DB 541 GGAACCTAGATCATCAGTCACCGAAGGTCCTACAGGGGCACAACTGCCCGCCACAAAC 600
QY 601 CCACCCCGCTTCGTAAGTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTT 660
|||||
DB 601 CCACCCCGCTTCGTAAGTTCATTTAGAAAATAGAGCTTTTAAAAATGTCCTGCCCTTT 660
QY 661 AACGTAGATATAAGCCTTCCCCACCTACCGTAATGTCATTTATATATATATATA 720
|||||
DB 661 AACGTAGATATAAGCCTTCCCCACCTACCGTAATGTCATTTATATATATATATA 720
QY 721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTT 780
|||||
DB 721 TTCTTATAAAATGTAAGAAAGAAAACACCGCTTCTGCTTTTCACTGTGTGGAGTTT 780
QY 781 TCTGGAGTGAGCACTCACGCCCTTAAGCGACATTCATGTGGGCAATTCCTGCGAGCCTCG 840
|||||
DB 781 TCTGGAGTGAGCACTCACGCCCTTAAGCGACATTCATGTGGGCAATTCCTGCGAGCCTCG 840
841 CAGCCTCCGGAAGCTGTCGACTTCATGACAAGCATTTTGTGAAGTGGGAAGCTCAGGGG 900
|||||
DB 841 CAGCCTCCGGAAGCTGTCGACTTCATGACAAGCATTTTGTGAAGTGGGAAGCTCAGGGG 900
QY 901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960
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DB 901 GGTACTGCTCTCTTTGAGTCACACTGCTAGCAAAATGGCAGAACCAAGCTCAAAATAA 960
961 AATAAAATATTATTTCACTTCACTCAAAAAA 994
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Db 961 AATAAATTATTTTCATTCATTCACCTCAAAAAA 994

RESULT 6
US-08-474-177-36
; Sequence 36, Application US/08474177
; Patent No. 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "Splice site acceptor."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 458
; OTHER INFORMATION: /note= "Splice site acceptor."

US-08-474-177-36

Query Match 94.9%; Score 943.8; DB 1; Length 947;
Best Local Similarity 99.8%; Pred. No. 3e-213;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 41 ATGGATCCGGCGGGGAGCAGCATGGAGCCCTTCGGCTGACTGGCTGGCCACGCGCGCG 100
Db 1 ATGGAGCCGGCGGGGAGCAGCATGGAGCCCTTCGGCTGACTGGCTGGCCACGCGCGCG 60
QY 101 GCCCGGGGTCCGGTAGAGAGGTGCGGGCGCTCTGGAGCGCTGGCGTGCCTCCACGCA 160
Db 61 GCCCGGGGTCCGGTAGAGAGGTGCGGGCGCTCTGGAGCGCGGGGGCGCTGCCCAACGCA 120
QY 161 CCGAATAGTTACGTCGGAGCGCCGATCCAGGTTCATGATGGCGAGCGCCCGAGTGGCG 220
Db 121 CCGAATAGTTACGTCGGAGCGCCGATCCAGGTTCATGATGGCGAGCGCCCGAGTGGCG 180
QY 221 GAGCTGCTGCTCCACGGCGGGAGCCCACTGGCGGACCCCGCCACTCTCAACCCGA 280
Db 181 GAGCTGCTGCTCCACGGCGGGAGCCCACTGGCGGACCCCGCCACTCTCAACCCGA 240
QY 281 CCGTGCACGACGCTGCCGGGAGGCTTCTTGACACGCTGCTGCTGCACCGGCC 340
Db 241 CCGTGCACGACGCTGCCGGGAGGCTTCTTGACACGCTGCTGCTGCACCGGCC 300
QY 341 GGGGCGGCTGGACGTGGCGATGCTGGGGCGCTGCTGCCCTGGACCTGGCTGAGGAG 400
Db 301 GGGGCGGCTGGACGTGGCGATGCTGGGGCGCTGCTGCCCTGGACCTGGCTGAGGAG 360
QY 401 CTGGGCGATCGGATGTGGACGGTACTGTGGCGGGCTGCGGGGGGCGACCGAGGCGAGT 460
Db 361 CTGGGCGATCGGATGTGGACGGTACTGTGGCGGGCTGCGGGGGGCGACCGAGGCGAGT 420
QY 461 AACCATGCCGCGATAGTCCCGGAGGTCCCTCAGACATCCCGCATTTGAAAGAACCCAG 520
Db 421 AACCATGCCGCGATAGTCCCGGAGGTCCCTCAGACATCCCGCATTTGAAAGAACCCAG 480
QY 521 AGAGGCTCTGAGAACTCGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 580
Db 481 AGAGGCTCTGAGAACTCGGAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 540
QY 581 ACAACTGCCCGCCGACACCCCGCTTCGTAGTTTCATTTAGAAAAATAGAGCTT 640
Db 541 ACAACTGCCCGCCGACACCCCGCTTCGTAGTTTCATTTAGAAAAATAGAGCTT 600
QY 641 TTAATAATGTCCTGCTTTAAGCTAGATATAAGCTTCCCGCACTACCGTAATGTCCA 700
Db 601 TTAATAATGTCCTGCTTTAAGCTAGATATAAGCTTCCCGCACTACCGTAATGTCCA 660
QY 701 TTTATATCAATTTTATATATTTTATAAAATGTAAAAAAGAAAAACACCGCTTCTGCC 760
Db 661 TTTATATCAATTTTATATATTTTATAAAATGTAAAAAAGAAAAACACCGCTTCTGCC 720
QY 761 TTTTCACTGTGTGGAGTTTCTGGAGTGAGCACTACGCGCTTAAGCGCACATTCATGTG 820
Db 721 TTTTCACTGTGTGGAGTTTCTGGAGTGAGCACTACGCGCTTAAGCGCACATTCATGTG 780
QY 821 GGCATTTCTTGGAGCTCGCAGCCTCCGGAAGCTGTGACATTCATGACAAGCATTTTGT 880
Db 781 GGCATTTCTTGGAGCTCGCAGCCTCCGGAAGCTGTGACATTCATGACAAGCATTTTGT 840
QY 881 GAAGTAGGAAGCTCAGGGGGTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGCG 940
Db 841 GAAGTAGGAAGCTCAGGGGGTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGCG 900
QY 941 AGAACCAAGCTCAATATAAAATATAAATTTTTCATTTCATTCATC 987
Db 901 AGAACCAAGCTCAATATAAAATATAAATTTTTCATTTCATTCATC 947

RESULT 7

US-08-487-033-36
; Sequence 36, Application US/08487033
; Patent No. 573927
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "Splice site acceptor."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 458
; OTHER INFORMATION: /note= "Splice site acceptor."
; US-08-487-033-36

Query Match 94.9%; Score 943.8; DB 2; Length 947;
Best Local Similarity 99.8%; Pred. No. 3e-213;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	41	ATGGATCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGCCGG	100
Db	1	ATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGCCGG	60
QY	101	GCCCGGGGTCTGGGTAGAGGAGGTGCGGGCGCTGCTGAGGCGGTGGCGTGCCTCAACGCA	160
Db	61	GCCCGGGGTCTGGGTAGAGGAGGTGCGGGCGCTGCTGAGGCGGGGGCGCTGCCCAACGCA	120
QY	161	CGAATAGTTACGGTCGGAGCGCATCCAGGTCATGATGATGGCAGCCCGAGTGGCG	220
Db	121	CGAATAGTTACGGTCGGAGCGCATCCAGGTCATGATGATGGCAGCCCGAGTGGCG	180
QY	221	GAGCTGCTGCTGCTCCACGGCGGGAGCCCACTGCGCCGACCCCGCCACTCTCACCCGA	280
Db	181	GAGCTGCTGCTGCTCCACGGCGGGAGCCCACTGCGCCGACCCCGCCACTCTCACCCGA	240
QY	281	CCCGTCACGACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGACACCGGGCC	340
Db	241	CCCGTCACGACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGACACCGGGCC	300
QY	341	GGGGCGGCTGGACGTGCGCGATGCTGGGGCGGTCTGCCGGTGGACCTGGCTGAGGAG	400
Db	301	GGGGCGGCTGGACGTGCGCGATGCTGGGGCGGTCTGCCGGTGGACCTGGCTGAGGAG	360
QY	401	CTGGCCATCGCGATGCTCGCACGGTACCTGCGCGCGGGCTGCGGGGGGCGCAGGAGCAGT	460
Db	361	CTGGCCATCGCGATGCTCGCACGGTACCTGCGCGCGGGCTGCGGGGGGCGCAGGAGCAGT	420
QY	461	AACCATGCCCGCATAGATGCCGGGAAGTCCCTCAGACATCCCGATGAAAGAACCCAG	520
Db	421	AACCATGCCCGCATAGATGCCGGGAAGTCCCTCAGACATCCCGATGAAAGAACCCAG	480
QY	521	AGAGGCTCTGAGAAACCTCGGAAACTTAGATCATCAGTCACCGAAGGTCTCTACAGGGCC	580
Db	481	AGAGGCTCTGAGAAACCTCGGAAACTTAGATCATCAGTCACCGAAGGTCTCTACAGGGCC	540
QY	581	ACACTGCCCCCGCCACACCCACCCCGCTTCGTTAGTTTCATTAGAAAATAGAGCTT	640
Db	541	ACACTGCCCCCGCCACACCCACCCCGCTTCGTTAGTTTCATTAGAAAATAGAGCTT	600
QY	641	TTAAAAATGTCCTGCCCTTTTAACTAGATATAGCCTTCCCCCACCACCGTAATGTCCA	700
Db	601	TTAAAAATGTCCTGCCCTTTTAACTAGATATAGCCTTCCCCCACCACCGTAATGTCCA	660
QY	701	TTTATATCATTTTATATATTTTATATAATTTTATATAATTTTATATAATTTTATATAAT	760
Db	661	TTTATATCATTTTATATATTTTATATAATTTTATATAATTTTATATAATTTTATATAAT	720
QY	761	TTTTCACGTGTTGGAGTTTCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTG	820
Db	721	TTTTCACGTGTTGGAGTTTCTGGAGTGAGCACTCACGCCCTTAAGCGCACATTCATGTG	780
QY	821	GGCATTTCTTGGAGCCTCGCAGCCTCCCGAAGCTCTCGACTTCATGACAAGCATTTTGT	880
Db	781	GGCATTTCTTGGAGCCTCGCAGCCTCCCGAAGCTCTCGACTTCATGACAAGCATTTTGT	840
QY	881	GAACTAGGAAGCTCAGGGGGTTACTGGCTTCTTTAGTACACTGCTGAGCAATGGC	940
Db	841	GAACTAGGAAGCTCAGGGGGTTACTGGCTTCTTTAGTACACTGCTGAGCAATGGC	900
QY	941	AGAACCAAGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	987
Db	901	AGAACCAAGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	947

RESULT 8
US-08-480-810-36
; Sequence 36, Application US/08480810
; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 151
OTHER INFORMATION: /note= "splice site acceptor."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 458
OTHER INFORMATION: /note= "splice site acceptor."

Query Match 94.9%; Score 943.8; DB 2; Length 947;
Best Local Similarity 99.8%; Pred. No. 3e-213;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 41 ATGGATCGCGCGCGGAGCAGCATGAGCGCTTCGGCTGACTGCTGCCACGCCCGCG 100
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Db 1 ATGGAGCGCGCGCGGAGCAGCATGAGCGCTTCGGCTGACTGCTGCCACGCCCGCG 60
Qy 101 GCCCGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGTGCGCGCTGCCCNACGCA 160

Db 61 GCCCGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGGGCGCTGCCCAACGCA 120
Qy 161 CCGAATAGTTACGGTCGAGAGCCGATCCAGTCTATGATGATGGCAGCGCCGAGTGGCG 220
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Db 181 GAGCTGCTGTCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCACTCTCACCCGA 240
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Qy 341 GGGCGGGGTGGACGTCGCGATGCTGGGGCGCTGTCGCCGTGGACCTGGCTGAGGAG 400
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Db 301 GGGCGGGGTGGACGTCGCGATGCTGGGGCGCTGTCGCCGTGGACCTGGCTGAGGAG 360
Qy 401 CTGGGCCATCGCGATGTCGACGGTACTGCGCGCGGTGCGGGGGGACACAGAGGAGT 460
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Db 361 CTGGGCCATCGCGATGTCGACGGTACTGCGCGCGGTGCGGGGGGACACAGAGGAGT 420
Qy 461 AACCATGCCCGCATAGATGCCGCGAGGTCCCTCAGACATCCCGGATGGAAGAACGAG 520
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Db 421 AACCATGCCCGCATAGATGCCGCGAGGTCCCTCAGACATCCCGGATGGAAGAACGAG 480
Qy 521 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGTCACCGAAAGTCTCAGAGGCC 580
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Db 481 AGAGGCTCTGAGAAACCTCGGGAACTTAGATCATCATGTCACCGAAAGTCTCAGAGGCC 540
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Db 661 TTTATATCATTTTTTATATATTTTATAAATAATGTAATAAAGAAAAACACCGCTTCTGCC 720
Qy 761 TTTTCACTGTTGGAGTTTCTGGAGTGAGCACTACGCGCTAAGCGCAATCATGTG 820
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Qy 821 GGCATTTCTTCGGAGCTCGAGCTCCGGAAGCTGTCGACTTCATGACAGCAATTTGT 880
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Db 781 GGCATTTCTTCGGAGCTCGAGCTCCGGAAGCTGTCGACTTCATGACAGCAATTTGT 840
Qy 881 GAACTAGGGAAGCTCAGGGGGTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGGC 940
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Db 841 GAACTAGGGAAGCTCAGGGGGTTACTGGCTTCTTTGAGTCACACTGCTAGCAAAATGGC 900
Qy 941 AGAACCAAGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 987
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RESULT 9
US-08-508-735-36
; Sequence 36, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000

;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/508,735
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US to be assigned
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03316
;; FILING DATE: 17-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4848
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 947 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 151
;; OTHER INFORMATION: /note= "Splice site acceptor."
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 458
;; OTHER INFORMATION: /note= "Splice site acceptor."
;;
;; US-08-508-735-36

Query Match 94.9%; Score 943.8; DB 3; Length 947;
Best Local Similarity 99.8%; Pred. No. 3e-213; 2; Indels 0; Gaps 0;
Matches 945; Conservative 0; Mismatches 0;
QY 41 ATGGATCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCGCG 100
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Db 1 ATGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCGCG 60
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Db 61 GCCCGGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGAGAGCGGTGGCGTGCACAGCA 120
QY 161 CCAGTAGTTACGGTCCGAGGCCGATCCAGGTCTATGATGATGGCAGCGCCGAGTGGCG 220
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Db 121 CCAGTAGTTACGGTCCGAGGCCGATCCAGGTCTATGATGATGGCAGCGCCGAGTGGCG 180
QY 221 GAGTGTGCTGTCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA 280
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Db 181 GAGTGTGCTGTCTCCACGGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA 240
QY 281 CCGGTGCACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGCACCGGGGCC 340
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QY 341 GGGCGCGCGCTGGACGTGCGCGGATGCCTGGGGCGGTCTGCCCGTGGACCTGGCTGAGGAG 400

Db 301 GGGCGCGCGCTGGACGTGCGCGATGCTGGGGCGGTCTGCCCGTGGACCTGGCTGAGGAG 360
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Db 361 CTGGGCCATCGCGATGTCGCACCGGTACCTGCGCGCGGTGCGGGGGGCGCACGAGGCGAGT 420
QY 461 AACCATGCCCGCATAGATGCCGGGAAGGTCCCTCAGACATCCCCCGATTGAAAGAACGAG 520
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Db 421 AACCATGCCCGCATAGATGCCGGGAAGGTCCCTCAGACATCCCCCGATTGAAAGAACGAG 480
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QY 581 ACAACTGCCCGCCGCCACACCCACCGCTTTCGTAGTTTTCATTAGAAAATAGAGCTT 640
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Db 601 TTAATAATGTCCTGCGCTTTTAACGTAGATATAAGCCTTCCCCCAGCTACCGTAATGTCCA 660
QY 701 TTTATATCATTTTATATATTTTATATAATCTTATAAAATGTAAAAAGAAACACCGCTTCTGCC 760
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Db 661 TTTATATCATTTTATATATTTTATATAATCTTATAAAATGTAAAAAGAAACACCGCTTCTGCC 720
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Db 781 GGCATTCTTCGAGCGCTCCGAGCCTCCGGAAGGTGCGACTTCATGACAGCAATTTGT 840
QY 881 GAACTAGGGAAGCTCAGGGGGTTACTGGCTTCTTGTAGTCACACTGCTAGCAAAATGGC 940
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Db 841 GAACTAGGGAAGCTCAGGGGGTTACTGGCTTCTTGTAGTCACACTGCTAGCAAAATGGC 900
QY 941 AGAACCAAGCTCAATAATAAAATTAATTTTTCATTTCATTCATTCACCTC 987
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Db 901 AGAACCAAGCTCAATAATAAAATTAATTTTTCATTTCATTCATTCACCTC 947

RESULT 10
US-08-848-251-36
; Sequence 36, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; METHOD OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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> APPLICATION NUMBER: US 08/474,083
> FILING DATE: 07-JUN-1995
> APPLICATION NUMBER: PCT/US95/03537
> FILING DATE: 17-MAR-1995
> PRIORITY DATA:
> APPLICATION NUMBER: US 08/251,938
> FILING DATE: 01-JUN-1994
> PRIORITY DATA:
> APPLICATION NUMBER: US 08/215,087
> FILING DATE: 18-MAR-1994
> PRIORITY DATA:
> APPLICATION NUMBER: US 08/215,086
> FILING DATE: 18-MAR-1994
> PRIORITY DATA:
> APPLICATION NUMBER: US 08/227,369
> FILING DATE: 14-APR-1994
> PRIORITY DATA:
> APPLICATION NUMBER: US 08/214,582
> FILING DATE: 18-MAR-1994
> ATTORNEY/AGENT INFORMATION:
> NAME: Ihnen, Jeffrey L.
> REGISTRATION/DOCKET NUMBER: 28,957
> REFERENCE/DOCKET NUMBER: 24884-109348-G
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 202-962-4810
> TELEFAX: 202-962-8300
> INFORMATION FOR SEQ ID NO: 36:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 947 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: double
> TOPOLOGY: linear
> MOLECULE TYPE: cDNA
> HYPOTHEetical: NO
> ANTI-SENSE: NO
> ORIGINAL SOURCE:
> ORGANISM: Homo sapiens
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: 151
> OTHER INFORMATION: /note= "Splice site"
> FEATURE:
> NAME/KEY: misc_feature
> LOCATION: 458
> OTHER INFORMATION: /note= "Splice site"
> US-08-848-251-36

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Query Match	94.9%	Score	943.8	DB	4	Length	947
Best Local Similarity	99.8%	Pred. No.	3e-213				
Matches	945	Conservative	0	Mismatches	2	Indels	0
Gaps	0						
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Db	61	GCCC	GGGCTCGGGTAGAGAGGTGCGGCGCTGCTGGAGGGGGGGCGTGCCCAACGCA	120			
QY	161	CCGA	ATAGTTACGGTCGGAGCCGATCAGGTCTATGATGATGGGCAGCCCGAGTGGCG	220			
Db	121	CCGA	ATAGTTACGGTCGGAGCCGATCAGGTCTATGATGATGGGCAGCCCGAGTGGCG	180			
QY	221	GAG	CTGCTGCTCCACGGCGGGAGCCCAACTCGCGCGACCCCGGCACCTCTCACCGGA	280			
Db	181	GAG	CTGCTGCTCCACGGCGGGAGCCCAACTCGCGCGACCCCGGCACCTCTCACCGGA	240			
QY	281	CCG	TGACAGAGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGGGCC	340			
Db	241	CCG	TGACAGAGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGGGCC	300			
QY	341	GGG	CGGGGCTGGACGTGCGCGGATGCTCTGGGGCGGCTCTGCCCGTGGAGCTGGCTGAGGAG	400			

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RESULT 11
US-08-486-047-36
; Sequence 36, Application US/08486047
; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938

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;; FILING DATE: 01-JUN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,087
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/215,086
;; FILING DATE: 18-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,369
;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Innen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 36:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 947 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 151
;; OTHER INFORMATION: /note= "Splice site acceptor."
;; FEATURE:
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;; LOCATION: 458
;; OTHER INFORMATION: /note= "Splice site acceptor."
US-08-486-047-36

Query Match 94.9%; Score 943.8; DB 4; Length 947;
Best Local Similarity 99.8%; Pred. No. 3e-213;
Matches 945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 ATGGATCCGGCGGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCGCCAGCGCGCG 100
DB 1 ATGGAGCCGGCGGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCGCCAGCGCGCG 60
QY 101 GCCCGGGGTGGGTAGAGGAGGTGGCGGCGCTGCTGGAGCGGTGGCGTGCACCGCA 160
DB 61 GCCCGGGGTGGGTAGAGGAGGTGGCGGCGCTGCTGGAGCGGTGGCGTGCACCGCA 120
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DB 301 GGGCGCGGTGACGTGGCGGATGCTGGGGCGGTGCTGCCCTGACCTGGCTGAGGAG 360
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DB 361 CTGGGGCATCGGATCTCGACGCTACCTGCGCGGGCTGCGGGGGGACACGAGGCGAGT 420

QY 461 AACATGCCCGCATAGATGCGCGGGAAGTCCCTCAGACATCCCGATTGAAAGAACAG 520
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QY 521 AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTCACGGAAGTCTTACAGGGCC 580
DB 481 AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTCACGGAAGTCTTACAGGGCC 540
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QY 941 AGAACCAAGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 987
DB 901 AGAACCAAGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 947

RESULT 12
US-09-120-130-36
; Sequence 36, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,130
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086

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, FILING DATE: 18-MAR-1994 '
, PRIOR APPLICATION DATA: '
, APPLICATION NUMBER: US 08/227,369
, FILING DATE: 14-APR-1994
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/214,582
, FILING DATE: 18-MAR-1994
, ATTORNEY/AGENT INFORMATION:
, NAME: Inhen, Jeffrey L.
, REGISTRATION NUMBER: 28,957
, REFERENCE/DOCKET NUMBER: 24884-109348
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 202-962-4810
, TELEFAX: 202-962-8300
, INFORMATION FOR SEQ ID NO: 36:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 947 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
, MOLECULE TYPE: cDNA
, HYPOTHETICAL: NO
, ANTI-SENSE: NO
, ORIGINAL SOURCE:
, ORGANISM: Homo sapiens
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: 151
, OTHER INFORMATION: /note= "splice site"
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: 458
, OTHER INFORMATION: /note= "splice site"
US-09-120-130-36

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RESULT 13
US-09-115-252-36
; Sequence 36, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: WTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,252
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994


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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24984-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 151
; OTHER INFORMATION: /note= "Splice site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 458
; OTHER INFORMATION: /note= "Splice site"
;
US-09-115-252-36

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Query Match 94.9%; Score 943.8; DB 5; Length 947;

Query Match 94.9%; Score 943.8; DB 5; Length 947;

Query Match 94.9%; Score 943.8; DB 5; Length 947;

		Matches	945	Conservative	0	Mismatches	0	2	Indels	0	Gaps
QY	41	ATGGATCCGGCGCGGGAGCAGCATGAGCCCTTGGCTGACTGGCTGGCCACGCCGCG	100								
Db	1	ATGGAGCCGGCGGGAGCAGCATGAGCCTTGGCTGACTGGCTGGCCACGCCGCG	60								
QY	101	GCCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGGTGGCGTGCCTCACACGA	160								
Db	61	GCCCCGGGTGGGTAGAGAGGTGCGGGGCGCTGCTGGAGCGGGGCGTGCCTCACACGA	120								
QY	161	CGAATAGTTACGGTCGGAGGCCGATCCAGGTGTCATGATGATGGCAGCGCCGAGTGGCG	220								
Db	121	CGAATAGTTACGGTCGGAGGCCGATCCAGGTGTCATGATGATGGCAGCGCCGAGTGGCG	180								
QY	221	GAGCTGCTGCTGTCCACGGCGGGAGCCCAACTGCGCGACCCGCCCACTCTCACCCGA	280								
Db	181	GAGCTGCTGCTGTCCACGGCGGGAGCCCAACTGCGCGACCCGCCCACTCTCACCCGA	240								
QY	281	CCGTCACAGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGACCGGGCC	340								
Db	241	CCGTCACAGACGCTCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGACCGGGCC	300								
QY	341	GGGGCGGCTGACGCTGGCGGATGCTGGGGCCGTCCTCCGCTGGACCTGCTCAGGAG	400								
Db	301	GGGGCGGCTGACGCTGGCGGATGCTGGGGCCGTCCTCCGCTGGACCTGCTCAGGAG	360								
QY	401	CTGGGCCATCGCATGTCGCACGGTACCTGCGCGGGCTCGGGGGGACACAGAGGCACT	460								
Db	361	CTGGGCCATCGCATGTCGCACGGTACCTGCGCGGGCTCGGGGGGACACAGAGGCACT	420								
QY	461	AACCATGCCGCGATAGATGCCGGGAGGTCCCTCAGACATCCCCGATTGAAGAACCG	520								
Db	421	AACCATGCCGCGATAGATGCCGGGAGGTCCCTCAGACATCCCCGATTGAAGAACCG	480								
QY	521	AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTCACCGAGGTCCCTACAGGGCC	580								
Db	481	AGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCAGTCACCGAGGTCCCTACAGGGCC	540								
QY	581	ACAACCTGCCCGCCCAACAACCCACCCCGCTTTTCGTAGTTTTCATTAGAAAAATAGAGCTT	640								

[illegible]

RESULT 14

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US-08-154-915-3
Sequence 3, Application US/08154915
Patent No. 5618669
GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Xiong, Yue
TITLE OF INVENTION: Cyclin Complex Rea
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER RELATED FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,915
FILING DATE: 19-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

```

;; INFORMATION FOR SEQ ID NO: 3:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 948 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: both

;; TOPOLOGY: linear

;; MOLECULE TYPE: CDNA

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: 19..465

;; US-08-154-915-3

Query Match

Best Local Similarity 94.3%; Score 937.6; DB 1; Length 948;

Matches 940; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 5 CGGCACGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGCGGGGTC 64
QY 111 GGGTAGAGGAGTGCGGCGCTGTGTGGAGCGGTGGCGCTGCCAAACGACCCGAATAGTT 170
DB 65 GGGTAGAGGAGTGCGGCGCTGTGTGGAGCGGTGGCGCTGCCAAACGACCCGAATAGTT 124
QY 171 ACGGTGCGAGCGGATCATGATGATGGGAGCGCGCGCGCGCGCGGAGCTGTGTC 230
DB 125 ACGGTGCGAGCGGATCATGATGATGGGAGCGCGCGCGCGCGGAGCTGTGTC 184
QY 231 TGTCTCCACGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 290
DB 185 TGTCTCCACGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGGTC 244
QY 291 ACGGTGCGCGGAGCGGCTTCCTGGACACGCTGGTGGTGTGGCTGACCGCGCGCGCGCGGTC 350
DB 245 ACGGTGCGCGGAGCGGCTTCCTGGACACGCTGGTGGTGTGGCTGACCGCGCGCGCGCGGTC 304
QY 351 TGGACGTGCGCGATGCGTGGGCGCGCTGTGCCCGTGGACCTGGGTGAGGAGCTGGGCGATC 410
DB 305 TGGACGTGCGCGATGCGTGGGCGCGCTGTGCCCGTGGACCTGGGTGAGGAGCTGGGCGATC 364
QY 411 GCGATGTGCGACGCTTACCTGCGCGCGGCTGCGCGCGGCGCGCGCGCGCGCGCGCGCGCG 470
DB 365 GCGATGTGCGACGCTTACCTGCGCGCGGCTGCGCGCGGCGCGCGCGCGCGCGCGCGCGCG 424
QY 471 GCATAGATGCGCGGAGGTCCTCAGACATCCCGGATGGAAGAACGACGAGGCTCTG 530
DB 425 GCATAGATGCGCGGAGGTCCTCAGACATCCCGGATGGAAGAACGACGAGGCTCTG 484
QY 531 AGAAACCTCGGGAACCTTAGATCATCATGACGACGAGGCGCGCGCGCGCGCGCGCGCGCG 590
DB 485 AGAAACCTCGGGAACCTTAGATCATCATGACGACGAGGCGCGCGCGCGCGCGCGCGCGCG 544
QY 591 CCGGCACAAACCGCGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAATATG 650
DB 545 CCGGCACAAACCGCGCTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAATATG 604
QY 651 CCTGCCCTTTAACGTAGATATAAGCTTCCCGCGCTTCCCGCGCTTCCCGCGCTTCCCGCGCT 710
DB 605 CCTGCCCTTTAACGTAGATATAAGCTTCCCGCGCTTCCCGCGCTTCCCGCGCTTCCCGCGCT 664
QY 711 TTTTATATATCTTATAAAATGTAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 770
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QY 771 GTTGAGTTTTCTGGAGTGAGCACTCAGCGCGCTAAGCGCACTTATGTGGGCAATTTCTT 830
DB 725 GTTGAGTTTTCTGGAGTGAGCACTCAGCGCGCTAAGCGCACTTATGTGGGCAATTTCTT 784
QY 831 GCGAGCCTCGCAGCCTCGGGAAGCTGTGAGCTTTCATGACAGCACTTTGTGAACCTAGGGA 890
DB 785 GCGAGCCTCGCAGCCTCGGGAAGCTGTGAGCTTTCATGACAGCACTTTGTGAACCTAGGGA 844
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QY 891 AGCTCAGGGGGTTACTGGCTTCTCTTGAGTCACACTGTAGCAATGGCAGAACCAAG 950
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RESULT 15

PCT-US93-09945-3

Sequence 3, Application PC/TUS9309945

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related

TITLE OF INVENTION: Thereto

NUMBER OF SEQUENCES: 4

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/09945

FILING DATE:

Prior Application DATA:

APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCT-1992

Prior Application DATA:

APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1992

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 948 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 19..465

PCT-US93-09945-3

Query Match

Best Local Similarity 94.3%; Score 937.6; DB 6; Length 948;

Matches 940; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 51 CCGCGGGGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGCGGGGTC 110
DB 5 CGGCACGAGCAGCATGGAGCTTCGGCTGACTGGCTGGCCACGCGCGCGCGGGGTC 64
QY 111 GGGTAGAGGAGTGCGGCGCTGTGGAGCGGTGGCGCTGCCCAACGACCCGAATAGTT 170
DB 65 GGGTAGAGGAGTGCGGCGCTGTGTGGAGCGGTGGCGCTGCCCAACGACCCGAATAGTT 124
QY 171 ACGGTGCGAGCGGATCCAGGTGATGATGGGAGCGCGCGCGCGGAGCTGTGTC 230
DB 125 ACGGTGCGAGCGGATCCAGGTGATGATGGGAGCGCGCGCGGAGCTGTGTC 184
QY 231 TGTCTCCACGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGGTC 290
DB 185 TGTCTCCACGCGCGGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGGTC 244
QY 291 ACGGTGCGCGGAGCGGCTTCCTGGACACGCTGGTGGTGTGGCTGACCGCGCGCGCGGTC 350
DB 245 ACGGTGCGCGGAGCGGCTTCCTGGACACGCTGGTGGTGTGGCTGACCGCGCGCGCGGTC 304
QY 351 TGGACGTGCGCGATGCGTGGGCGCGCTGTGCCCGTGGACCTGGGTGAGGAGCTGGGCGATC 410
DB 305 TGGACGTGCGCGATGCGTGGGCGCGCTGTGCCCGTGGACCTGGGTGAGGAGCTGGGCGATC 364
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Db 365 GCGATGTCGCACGGTACCTGCGCGCGCTGCGGGGGCCAGAGGCAGTAACCATGCC 424
QY 471 GCATAGATGCGGGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACAGAGAGGCTCTG 530
Db 425 GCATAGATGCGGGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACAGAGAGGCTCTG 484
QY 531 AGAAACCTCGGGAACTTAGATCATAGTCACCGAAGGTCCTACAGGGCCACACTGCC 590
Db 485 AGAAACCTCGGGAACTTAGATCATAGTCACCGAAGGTCCTACAGGGCCACACTGCC 544
QY 591 CCGCCACACCCACCCCGCTTCGTAGTTCATTTAGAAAATAGAGCTTTTAAATGT 650
Db 545 CCGCCACACCCACCCCGCTTCGTAGTTCATTTAGAAAATAGAGCTTTTAAATGT 604
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QY 711 TTTTATATATCTTATAAAATGTAAAAAGAAAAACACCGCTTCGTGCTTTTCACTGT 770
Db 665 TTTTATATATCTTATAAAATGTAAAAAGAAAAACACCGCTTCGTGCTTTTCACTGT 724
QY 771 GTTGGAGTTTCTGGAGTGAAGCTACGCGCTAAGCGCACATTCATGTGGCATTTCTT 830
Db 725 GTTGGAGTTTCTGGAGTGAAGCTACGCGCTAAGCGCACATTCATGTGGCATTTCTT 784
QY 831 GCGAGCCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACACAGCATTTTGTGAAGTGGGA 890
Db 785 GCGAGCCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACACAGCATTTTGTGAAGTGGGA 844
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QY 951 CTCAAATAAAAAATAAATTTTTCATTTCATTCCTCAAAAAA 994
Db 905 CTCAAATAAAAAATAAATTTTTCATTTCATTCCTCAAAAAA 948

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 00:08:05 ; Search time 1049.06 Seconds
(without alignments)
4178.378 Million cell updates/sec

Title: US-09-016-869A-1
Perfect score: 994
Sequence: 1 CGGAGAGGGGAGACAGAC.....CATTCATCTACTCAAAAAA 994

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: em_est2:*
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122: gb_gss18:*
123: gb_gss19:*
124: em_gss13:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	625.2	62.9	679	38	AI379336 tc73403.x
C 3	560	56.3	568	79	AW664294 h109c04.x
C 4	558.6	56.2	566	39	AI394605 tq13q05.x
C 5	558.2	56.2	590	45	AI871381 w181d11.x
C 6	546.4	55.0	579	45	AI870879 w177d11.x
C 7	545.8	54.9	604	45	AI859822 w20n06.x
C 8	544.2	54.7	580	38	AI362049 qy39f07.x
C 9	543.8	54.7	579	36	AI198233 q155d12.x
C 10	535	53.8	729	44	AI817709 wk25c11.x
C 11	530	53.3	563	46	AI954684 w34h12.x
C 12	526	52.9	774	44	AI765096 w148n08.x
C 13	525.2	52.8	531	42	AI633790 tt28a10.x
C 14	523.2	52.6	528	45	AI885362 w192h04.x
C 15	522.8	52.6	528	42	AI638416 tt31q03.x
C 16	522.4	52.6	708	38	AI363262 qy56f03.x
C 17	521.2	52.4	579	62	AW006218 w293q05.x
C 18	519	52.2	648	71	AW328496 ds02h12.x
C 19	518.6	52.2	599	28	AA557137 n174d05.s
C 20	484.8	48.8	531	44	AI806771 w15a09.x
C 21	483	48.6	505	36	AI186333 q30a08.x
C 22	482.8	48.6	496	71	AW328497 ds02h12.y
C 23	464.2	46.7	494	69	AW190459 x115e01.x
C 24	463	46.6	533	32	AA877595 n17f06.s
C 25	460.4	46.3	531	33	AA946585 oq49e06.s
C 26	460.2	46.3	474	70	AW246625 z821b97.3
C 27	451.2	45.4	563	44	AI869175 w150c04.x
C 28	427	43.0	465	44	AI818660 wk89c11.x
C 29	426.8	42.9	450	35	AI091727 ow59q04.x
C 30	422.8	42.5	426	45	AI859893 w23a09.x
C 31	416.2	41.9	421	40	AI479957 tm73d10.x
C 32	407.4	41.0	419	46	AI937552 w78f11.x
C 33	406.6	40.9	454	21	AA098836 zn44e11.s
C 34	405.4	40.8	419	41	AI500223 tm94b03.x
C 35	403.6	40.6	417	39	AI454154 UT-R-BT0-
C 36	403.2	40.6	447	36	AI149429 gc72f05.x
C 37	399.2	40.2	441	20	AA055664 z175f06.s
C 38	398.8	40.1	532	20	AA069792 zml5a11.s
C 39	391	39.3	401	44	AI803069 tj47a12.x
C 40	380.6	38.3	398	34	AI040505 ox14f08.s
C 41	377.2	37.9	548	32	AA903110 ox52b03.s
C 42	371.8	37.4	410	21	AA076328 zml8a12.s
C 43	365.8	36.8	369	38	AI363480 qy69f05.x
C 44	364.8	36.7	395	36	AI199084 q140a06.x
C 45	362.8	36.5	374	28	AA579918 nm88a08.s

ALIGNMENTS

RESULT 1
LOCUS AI337358 689 bp mRNA EST 18-MAR-1999
DEFINITION tb98f09.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2062409 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR

A ; mRNA sequence.
AI337358
VERSION AI337358.1 GI:4074285
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 689)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036732.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 1023 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 469.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2062409"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1057416-106255, and 1144584-1145351)."
BASE COUNT 162 a 170 c 186 g 167 t 4 others
ORIGIN
Query Match 65.6%; Score 652.4; DB 38; Length 689;
Best Local Similarity 98.4%; Pred. No. 6.9e-149;
Matches 678; Conservative 0; Mismatches 9; Indels 2; Gaps 2;
Qy 296 GCCGGGAGGCTTCCTGGACACGCTGGTGTCTGCACCGCGCGCGGCTGCAC 355
Db 689 GCCGGGAGGCTTCCTGGACACCGCTGGTGTCTGCACCGCGCGCGGCTGCAC 630
Qy 356 GTGCGCATGCTGGGCGCGCTCTGCCGTGGACCTGTGGCTGAGGAGCTGGGCCATCGCGAT 415
Db 629 GTGCGCATGCTGGGCGCGCTCTGCCGTGGACCTGTGGCTGAGGAGCTGGGCCATCGCGAT 570
Qy 416 GTGCGAC-GGTACTGCGCGCGGCTGGGGGGGACCCAGAGGAGTAACTATGCCCGCAT 474
Db 569 GTGCGACGGGTACTGCGCGCGGCTGGGGGGGACCCAGAGGAGTAACTATGCCCGCAT 510
Qy 475 AGATGCCGCGAGAGTCCCTCAGACATCCCGGATTGAAGAACCCAGAGAGGCTCTGAGAA 534
Db 509 AGATGCCGCGAGAGTCCCTCAGACATCCCGGATTGAAGAACCCAGAGAGGCTCTGAGAA 450
Qy 535 ACCTCGGGAACCTTAGATCATCATAGTACCAGAGTCTCTACAGGGGCCACAA-CTGCCCCCG 593
Db 449 ACCTCGGGAACCTTAGATCATCATAGTACCAGAGTCTCTACAGGGGCCACAACTGCCCNCG 390

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QY 594 CCACACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTCT 653
Db 389 CCACACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAATGCTCT 330
QY 654 GCCTTTTAAAGCTAGATATAAGCCTTCCCCCACTACCGTAATGTCCTTATATATATATTT 713
Db 329 GCCTTTTAAAGCTAGATATAAGCCTTCCCCCACTACCGTAATGTCCTTATATATATTT 270
QY 714 TTATATATTTTAAATAATGTAATAAGAAACACCGCTTCGCTTTTCACTGTGTT 773
Db 269 TTATATATTTTAAATAATGTAATAAGAAACACCGCTTCGCTTTTCACTGTGTT 210
QY 774 GGAGTTTCTGGAGTAGAGCACTCACGCCCTAAGGCAATTCATGCGCAATTCCTTTCGCG 833
Db 209 GGAGTTTCTGGAGTAGAGCACTCACGCCCTAAGGCAATTCATGCGCAATTCCTTTCGCG 150
QY 834 AGCTCGCAGCCCTCCGGAAGCTGTGCACTTCATGACAAAGCATTTTGTGAAGTACGGAAGC 893
Db 149 AGCTCGCAGCCCTCCGGAAGCTGTGCACTTCATGACAAAGCATTTTGTGAAGTACGGAAGC 90
QY 894 TCAGGGGGTACTGCTTCTTGTAGTCACACTGTAGCAAAATGGCAGAACCAAGCTC 953
Db 89 TCAGGGGGTACTGCTTCTTGTAGTCACACTGTAGCAAAATGGCAGAACCAAGCTC 30
QY 954 AATAAAATAAATAATTTTCACTTATT 982
Db 29 AATAAAATAAATAATTTTCACTTATT 1

RESULT 2
AL1379336/c
LOCUS
DEFINITION
tc73g03.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070292
3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA
FORM ;, mRNA sequence.

ACCESSION
AL1379336
VERSION
AL1379336.1 GI:4189189
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Dec 5, 1997 this sequence version replaced gi:2662837.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
FEATURES
Location/Qualifiers
1..679
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2070292"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDH, pregnant uterus
NHPU, and fetal heart NBH19) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
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consisted of I.M.A.G.E. clones 260332-265223,
340488-345479, and 484488-489479."
BASE COUNT 158 a 154 c 178 g 182 t 7 others
ORIGIN

Query Match 62.9%; Score 625.2; DB 38; Length 679;
Best Local Similarity 97.0%; Pred. No. 2.9e-142;
Matches 644; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 331 GCACCGCGCGCGCGCGCTGGACGTGCGCATGCGTGGGGCGCTGCGCGTGGACCT 390
Db 673 GCACCGCGCGCGCGCGCTGGACGTGCGCATGCGTGGGGCGCTGCGCGTGGACCT 615
QY 391 GGTGAGGAGCTGGGCGCATCGCATGTGCGACGTGCGTGGGGCGCTGCGGGGGGCAC 450
Db 614 GCTGAGGAGCTGGGCAATCGCATGTGCGACGTGCGTGGGGCGCTGCGGGGGGCAC 555
QY 451 CAGAGGCACTAACCATGCCCGCATAGATGCCGGGAAGTCCCTCAGACATCCCGATTG 510
Db 554 CAGAGGCACTAACCATGCCCGCATAGATGCCGGGAAGTCCCTCAGACATCCCGATTG 495
QY 511 AAGAAGCCAGAGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCATGACCAAGGTC 570
Db 494 AAGAAGCCAGAGAGGCTCTGAGAAACCTCGGGAACCTTAGATCATCATGACCAAGGTC 435
QY 571 CTACAGGGCCACAACTGCCCGCCACACCCACCGCTTTCGTAGTTTTCATTTAGAA 630
Db 434 CTACAGGGCCACAACTGCCCGCCACACCCACCGCTTTCGTAGTTTTCATTTAGAA 375
QY 631 AATAGAGCTTTTAAAAATGCTCTGCTTTTAAAGTAGATATAAGCTTCCCGCACTACCG 690
Db 374 AATAGAGCTTTTAAAAATGCTCTGCTTTTAAAGTAGATATAAGCTTCCCGCACTACCG 315
QY 691 TAAATGTCATTTATATATATTTTATATATTTTATATATTTTATATATTTTATATATTT 750
Db 314 TAAATGTCATTTATATATTTTATATATTTTATATATTTTATATATTTTATATATTT 255
QY 751 CGCTTCTGCTTTTCACTGTGTTGGAGTTTCTGGAGTAGAGCACTCACGCCCTTAAGCGCA 810
Db 254 CGCTTCTGCTTTTCACTGTGTTGGAGTTTCTGGAGTAGAGCACTCACGCCCTTAAGCGCA 195
QY 811 CATCATGTGGGCAATTTCTTGGAGGCTCGCAGCTCCGGAAGCTGTCGACTTCATGACA 870
Db 194 CATTCATGTGGGCAATTTCTTGGAGGCTCGCAGCTCCGGAAGCTGTCGACTTCATGACA 135
QY 871 AGCATTTTGTGAAGTGGGAGCTCAGGGGGTTTACTGGCTTCTCTGAGTCACACTGCT 930
Db 134 AGCATTTTGTGAAGTGGGAGCTCAGGGGGTTTACTGGCTTCTCTGAGTCACACTGCT 75
QY 931 AGCAATGGCAGAACCAAGCTCAAAATAAAATTTTATTTTATTTTATTTTATTTTATTTT 990
Db 74 AGCAATGGCAGAACCAAGCTCAAAATAAAATTTTATTTTATTTTATTTTATTTTATTTT 15
QY 991 AAAA 994
Db 14 AAAA 11

RESULT 3
AL1379336/c
LOCUS
DEFINITION
tc73g03.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2971782 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.

ACCESSION
AL1379336
VERSION
AL1379336.1 GI:7456835
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 568)
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AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Jul 7, 1999 this sequence version replaced gi:5407043.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/hml/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
FEATURES Location/Qualifiers
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/clone="IMAGE:2971782"
/clone_lib="NCI-CGAP_GUI"
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tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site 1: SalI; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
Technologies."
BASE COUNT 144 a 118 c 149 g 157 t
ORIGIN
Query Match 56.3%; Score 560; DB 79; Length 568;
Best Local Similarity 99.1%; Pred. No. 2.2e-126;
Matches 563; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 416 GTCGACGGTACCTCGCGGGCTCGCGGGGCGCCAGGAGGAGTAACTGCGCGCAT 475
Db 568 GTCGACGGTACCTCGCGGGCTCGCGGGGCGCCAGGAGGAGTAACTGCGCGCAT 509
Qy 476 GATGCGCGGAGGTCCTCAGACATCCCGATTGAAGAACCCAGAGAGCTCTGAGAAA 535
Db 508 GATGCGCGGAGGTCCTCAGACATCCCGATTGAAGAACCCAGAGAGCTCTGAGAAA 449
Qy 536 CTTGCGGAACTTAGATCATCAGTCACCGAAGTCTTACAGGGCCACACCTGCCCGCC 595
Db 448 CTTGCGGAACTTAGATCATCAGTCACCGAAGTCTTACAGGGCCACACCTGCCCGCC 389
Qy 596 ACAACCCACCGCGTTTCGTAGTTTTCATTAGAAAATAGAGCTTTTAAAAATGTCCTGC 655
Db 388 ACAACCCACCGCGTTTCGTAGTTTTCATTAGAAAATAGAGCTTTTAAAAATGTCCTGC 329
Qy 656 CTTTAAAGTAGATATAGCTTCCCGACCTACCGTAATGTCCTATATATATATTTT 715
Db 328 CTTTAAAGTAGATATAGCTTCCCGACCTACCGTAATGTCCTATATATATATTTT 269
Qy 716 ATATATTTCTTAAAAATGTAAAAAGAAAACACCGCTTCTGCGCTTTTTCACGTGTGTGG 775
Db 268 ATATATTTCTTAAAAATGTAAAAAGAAAACACCGCTTCTGCGCTTTTTCACGTGTGTGG 209
Qy 776 AGTTTCTGGAGTAGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTGCAG 835
Db 208 AGTTTCTGGAGTAGAGCACTCACGCCCTTAAGCGCACATTCATGTGGGCAATTTCTTGCAG 149
Qy 836 CTTGCGACGCTCCGAGAGCTCTCGACTTCATCACAAGCATTTTGTGAAGTGGGAGCTC 895
Db 148 CTTGCGACGCTCCGAGAGCTCTCGACTTCATCACAAGCATTTTGTGAAGTGGGAGCTC 89
Qy 896 AGGGGGGTACTGGCTTCTCTTGTAGTCACTGCTAGCAAAATGGCAGAACCAAAAGCTCAA 955
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Db 88 AGGGGGTACTGCTTCTCTGTAGTCACACTGCTAGCAATGGCAGAACCAAAAGCTCAA 29
Qy 956 ATAAAAATAAAATATATTTTCATTCATTC 983
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Db 28 ATAAAAATAAAATAATTTTCATTCATTC 1
RESULT 4
AI394605/c 566 bp mRNA EST 30-MAR-1999
LOCUS t913905.x1 NCI-CGAP-CLL1 Homo sapiens cDNA clone IMAGE:2108696 3'
DEFINITION similar to SW:CDN2.HUMAN P42711 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A: contains LTR9.B3 TAR1 repetitive element;; mRNA sequence.
AI394605
ACCESSION AI394605.1 GI:4224152
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 755 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2108696"
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/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCATTCCTTTTTCCTTTTTCCTTTTTCCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 113 a 159 c 175 g 118 t 1 others
ORIGIN
Query Match 56.2%; Score 558.6; DB 39; Length 566;
Best Local Similarity 99.1%; Pred. No. 4.8e-126;
Matches 561; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 170 TACGTCGGAGCGCATCCAGGTCATGATGGCGCGCCGAGTGGCGAGCTGCTG 229
Db 566 TACGTCGGAGCGCATCCAGGTCATGATGGCGCGCGGAGTGGCGAGCTGCTG 507
Qy 230 CTGCTCACGCGCGGAGCCCACTGGCGGACCCCGCCACTCTCACCCGCCGTCGAC 289
Db 506 CTGCTCACGCGCGGAGCCCACTGGCGGACCCCGCCACTCTCACCCGCCGTCGAC 447
Qy 290 GACGCTGCCGGGAGGCTTCTCTGGACACGCTGTGTGTGCTGACCGCGCGGGCGGG 349
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Db 10 AAATGATAAAA 1
RESULT 12
AI765096/c
LOCUS
DEFINITION
w148D08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
Similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.b3 MER22 repetitive element ;, mRNA sequence.
ACCESSION
AI765096
VERSION
AI765096.1 GI:5231605
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/Image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 400.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/notes="Organ: Colon; Vector: pT7f3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaudo. "
BASE COUNT 153 a 220 c 221 g 179 t 1 others
ORIGIN
Query Match 52.9%; Score 526; DB 44; Length 774;
Best Local Similarity 86.0%; Pred. No. 4.4e-118;
Matches 583; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
Qy 72 CTTCCGGCTGACTGGTGGCCACGGCCGGGGTGGTGGGTAGAGGAGTGGCGGCGC 131
Db 706 CATCCCGGGTTCAGGGGAGGTGGCGGCCACGGCCAGGGGGCGCCCGCTGTGGCCATC 647
Qy 132 TCGTGGAGCGGTGGCGTGGCCACGACGCAAGTAGTACGGTCGGAGCGCGATCCAGG 191
Db 646 GTGCTTATGCTATTGAGGAGCCACGCTTTAGGGCAGCAGCGCGCTTCTAGAACACGAG 587
Qy 192 TCATGATGATGGCAGCCCGGAGTGGGGAGTCTGCTGCTCCACGCGCGGAGGCCA 251
Db 586 TCATGATGATGGCAGCCCGGAGTGGGGAGTCTGCTGCTCCACGCGCGGAGGCCA 527

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QY 635 GAGCTTTTAAATGTCCTGCTTTTACGTAGATATAGCCCTCCCGCACTACCGTAAA 694
|||||
Db 108 GAGCTTTTAAATGTCCTGCTTTTACGTAGATATAGCCCTCCCGCACTACCGTAAA 49
|||||
QY 695 TGTCATTATATCATTTTATATATTTCTTATATAAAATGTAAAAAG 742
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Db 48 TGTCCTTTATATCATTTTATATATTTCTTATATAAAATGTAAAAAG 1

RESULT 15
AI638416/c LOCUS
DEFINITION t131903.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3,
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.b3 TAR1 repetitive element ; , mRNA sequence.
ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528),
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/obrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 462.
FEATURES
source
location/Qualifiers
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2242420"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 163 g 114 t 2 others
ORIGIN

Query Match 52.6% Score 522.8; DB 42; Length 528;
Best Local Similarity 99.2% Pred No. 2.5e-117;
Matches 524; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 212 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGGCCCACTGCGCCGCCGCCACT 271
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Db 528 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGGCCCACTGCGCCGCCGCCACT 469
|||||
QY 272 CTCACCCGACCCGTCGACGAGCGTGCCTCCGCGGAGGGCTTCTTGGACAGCGTGGTGGCTG 331
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Db 468 CTCACCCGACCCGTGCACGACGCTGCCGCGAGGGTTCTCTGGACACGCTGSGTGTG 409
|||||
QY 332 CACCGGCGCGGGCGCGGCTGGACGTGCGCGATGCTGGGGCGGTCTGCCCGTGGACCTG 391
|||||
Db 408 CACCGGCGCGGGCGCGGCTGGACGTGCGCGATGCTGGGGCGGTCTGCCCGTGGACCTG 349
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QY 392 GCTGAGGAGCTGGGCCCATCGCGATGTGCGACGGTACCTGCGCGCGGTGCGGGGGGCACC 451
|||||
Db 348 GCTGAGGAGCTGGGCCCATCGCGATGTGCGACGGTACCTGCGCGCGGTGCGGGGGGCACC 289
|||||
QY 452 AGAGGAGTAAACATGCCCGCATAGATGCCGCGAAGGTCCTCAGACATCCCGCATTTGA 511
|||||
Db 288 AGAGGAGTAAACATGCCCGCATAGATGCCGCGAAGGTCCTCAGACATCCCGCATTTGA 229
|||||
QY 512 AAGAACCAGAGAGGCTCTGAGAAACCTCGGAAACCTTAGATCATCATGTCACCGAAGTCC 571
|||||
Db 228 AAGAACCAGAGAGGCTCTGAGAAACCTCGGAAACCTTAGATCATCATGTCACCGAAGTCC 169
|||||
QY 572 TACAGGCGCCAACTGCCCGCCGACAAACCCGCCGCTTTCGTAGTTTTCATTTAGAAA 631
|||||
Db 168 TACAGGCGCCAACTGCCCGCCGACAAACCCGCCGCTTTCGTAGTTTTCATTTAGAAA 109
|||||
QY 632 ATAGAGCTTTTAAAAATGCTGCTTTCCTTTTAACTAGATATATAAGCCCTCCCGCACTACCGT 691
|||||
Db 108 ATAGAGCTTTTAAAAATGCTGCTTTCCTTTTAACTAGATATATAAGCCCTCCCGCACTACCGT 49
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QY 692 AAATGTCCATTATATATATTTTATATATTTTATATATTTCTTATAAAATGTAAAA 739
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Db 48 AAATGTCCATTATATATATTTTATATATTTTATATATTTCTTATAAAATGTAAAA 1
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Job time: 9635 sec

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Date: Jul 21, 2000 8:05 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:
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-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -XGAPOP=6.500
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Search information block:

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Query length: 156

Database: GenEmbl.*

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ACCESSION AR037494
VERSION AR037494.1 GI:5955350
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kamb,A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 1 01-SEP-1998;
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ACCESSION AR062774
VERSION AR062774.1 GI:5990465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 1 01-DEC-1998;
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DEFINITION Sequence 1 from patent US 5624819.
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ORGANISM Unknown.
REFERENCE
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AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germline mutations in the MTS gene
JOURNAL Patent: US 5624819-A 1 29-APR-1997;
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ACCESSION AR001346
VERSION AR001346.1 GI:3963413
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 947)
AUTHORS Kamb,A.
TITLE MTS1E1.beta. gene
JOURNAL Patent: US 5739027-A 36 14-APR-1998;
FEATURES
Location/Qualifiers
source 1..947
/organism="unknown"
BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN
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alignment_scores:
Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718
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alignment_block:
US-09-016-869A-2 x AR001346 ..
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Align seg 1/1 to: AR001346 from: 1 to: 947

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1 ATGGAGCCGGCGGGGAGGAGCAGATGAGCCCTTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
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51 CACGGCCGGCGGGGCTGGGTAGAGAGGTGGGGCGCTGCTGGAGG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|| |||||||||||||||||||||||||||||||||||||||
101 CGGGGGCGCTGCCCAACGCCAGATAGTTACGGTCGGAGGCCGATCCAG 150
51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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151 GTCATGATGATGGGAGCGCCGAGTGGGGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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201 CGCGAGGCCCAACTGCGCGACCCGCCACTCTACCCGACCCGTCACG 250
84 sPAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|| |||||||||||||||||||||||||||||||||||||||
251 ACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTGGTGCACCGGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaTirPglyArgLeuProValAspLe 117
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301 GGGGGCGGGCTGGAGTGGCGCATGCCCTGGGGCCGCTGCTGCCCGTGACCT 350
117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
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351 GGCTGAGGAGCTGGGCCATCGCATGTCGACGGTACCTGCGCGGGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
||||:|||||||||||||||||||||||||||||||||||||||||
401 CGGGGGGACACAGAGCGAGTAAACCATGCCCGCATAGATGCCCGGAAGGT 450
151 ProSerAspIleProAsp 156
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451 CCTCAGACATCCCGAT 468
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seq_name: gb_pat:AR037526
seq_documentation_block:
LOCUS AR037526 947 bp DNA 29-SEP-1999
DEFINITION Sequence 36 from patent US 5801236.
ACCESSION AR037526
VERSION AR037526.1 GI:5955382
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 947)
AUTHORS Kamb,A.
TITLE Probes for MSL1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 36 01-SEP-1998;
FEATURES
Location/Qualifiers
source 1..947
BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

alignment_scores:
Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:
US-09-016-869A-2 x AR037526 ..
Align seg 1/1 to: AR037526 from: 1 to: 947

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
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1 ATGGAGCGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaAlaArgGlyArgValGluGluValAlaArgAlaLeuGluA 34
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51 CACGGCCCGCGCGCGGGGTGGGTAGAGAGGTGGCGGCGCTGCTGGAG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
||| |||||||||||||||||||||||||||||||||||||||
101 CGGGGGCGCTGCCCAAGCACCGCAATAGTTACGGTCGGAGCGCATCCAG 150
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
||||:|||||||||||||||||||||||||||||||||||||||||
151 GTCATGATGATGGCGACGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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201 CGGGAGCCCAACTGCGCCAGCCCGCCACTCTCACCCGACCCGTGCACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 ACGCTGCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCACCGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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301 GGGGCGGGCTGGACGTGGCGATGCTGGGGCGGTCTGCCCGTGGACCT 350
117 uAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134
||||:|||||||||||||||||||||||||||||||||||||||||
351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGGGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaAlaArgIleAspAlaGluGly 150
||||:|||||||||||||||||||||||||||||||||||||||||
401 CGGGGGCACACAGAGGCAGTAACCATGCCCGCATAGATGCCCGGAAGGT 450
151 ProSerAspIleProAsp 156
451 CCCTCAGACATCCCCGAT 468

seq_name: gb_pat:AR062806
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seq_documentation_block:
LOCUS AR062806 947 bp DNA 29-SEP-1999
DEFINITION Sequence 36 from patent US 5843756.
ACCESSION AR062806
VERSION AR062806.1 GI:5990497
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 947)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 36 01-DEC-1998;
FEATURES
Location/Qualifiers
source 1..947
BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

alignment_scores:
Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:
US-09-016-869A-2 x AR062806 ..
Align seg 1/1 to: AR062806 from: 1 to: 947

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||||:|||||||||||||||||||||||||||||||||||||||||
1 ATGGAGCGCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaAlaArgGlyArgValGluGluValAlaArgAlaLeuGluA 34
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51 CACGGCCCGCGCGCGGGGTGGGTAGAGAGGTGGCGGCGCTGCTGGAG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
||| |||||||||||||||||||||||||||||||||||||||
101 CGGGGGCGCTGCCCAAGCACCGCAATAGTTACGGTCGGAGCGCATCCAG 150
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
||||:|||||||||||||||||||||||||||||||||||||||||
151 GTCATGATGATGGCGACGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
||||:|||||||||||||||||||||||||||||||||||||||||
201 CGGGAGCCCAACTGCGCGAGCCCGCCACTCTCACCCGACCCGTGCACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 ACGCTGCCGGGAGGGCTTCCTGGACACGCTGGTGGTGTGTCACCGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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301 GGGGCGGGCTGGACGTGGCGATGCTGGGGCGGTCTGCCCGTGGACCT 350
117 uAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAla 134
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351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGGGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaAlaArgIleAspAlaGluGly 150
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401 CGGGGGCACACAGAGGCAGTAACCATGCCCGCATAGATGCCCGGAAGGT 450
151 ProSerAspIleProAsp 156
451 CCCTCAGACATCCCCGAT 468

seq_name: gb_pat:I41180
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seq_documentation_block:
LOCUS      I41180      947 bp      DNA
DEFINITION Sequence 36 from patent US 5624819.
ACCESSION I41180
VERSION   I41180.1  GI:2081770
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 947)
AUTHORS   Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE     Germ-line mutations in the MTS gene
JOURNAL   Patent: US 5624819-A 36 29-APR-1997;
FEATURES
     Location/Qualifiers
     source
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     /organism="unknown"
BASE COUNT 207 a 271 c 274 g 195 t
ORIGIN

alignment_scores:
  Quality: 789.00      Length: 156
  Ratio: 5.090        Gaps: 0
  Percent Similarity: 99.359  Percent Identity: 98.718

alignment_block:
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1 ATGGAGCGCGCGGGGAGCAGCATGGAGCCTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaArgGlyArgValGluValAlaArgAlaLeuGluA 34
|||||
51 CACGGCGCGCGCGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCACGACGCCAATAGTTACGGTCGGAGCGGATCCAG 150
51 ValMetMetGlySerAlaArgValAlaAlaGluLeuLeuLeuHisG1 67
|||||
151 GTCATGATGATGGCGAGCGCGGAGTGGCGAGCTGCTGCTCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84
|||||
201 CGCGGAGCCCACTCGCGCCACCCGCCACTCTCACCCGACCGGTGCACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGTCGGCGGAGGGTCTCTGGACACGCTGGTGGTGTGCTGCACCGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGCTGACGTCGCGATGCTGGGGCGCTGCTGGCGGTGACCT 350
117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
|||||
351 GGCTGAGGACGTGGCCATCGCATGTCGCACGGTACTGCGCGCGGCTG 400
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
|||||
401 CGGGGGCACCAGAGGAGTAACCATGCCGCATAGATGCCGCGGAAGGT 450
151 ProSerAspIleProAsp 156
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451 CCCTCAGACATCCCCGAT 468
seq_name: gb_pr2:HUMINK4X
seq_documentation_block:
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17 aThraAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34
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141 CGGGGGCGCTGCCCAACGACCGATAGTTACGGTCGGAGCGCATCCAG 190
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51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
|||||
191 GTCATGATGATGGGCGCGCGAGTGGCGAGCTGCTGCTCCACGG 240
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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241 CGCGAGCGCCAACTGCGCGGACCGCGCCACTCTCACCGACCGGTGCACG 290
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84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
291 ACGTGCGCGGGAGGGCTTCTTGACACGCTGGTGTGCTGCACCGGGCC 340
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
341 GGGCGCGCTGGACGTGCGGATGCTGGGGCGCTGCTGCCCGTGGACCT 390
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117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
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391 GCTGAGGAGCTGGGCCATTCGCGTGTGCGACGCTGGTGTGCTGCACGGCGTG 440
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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441 CGGGGGCACCAGAGGCGATACCATGCCGATAGATGCCGCGGAAGGT 490
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151 ProSerAspIleProAsp 156
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491 CCTCAGACATCCCGAT 508
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seq_name: gb_pat:167718

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seq_documentation_block: 1420 bp DNA PAT 30-DEC-1997
LOCUS I67718
DEFINITION Sequence 1 from patent US 5672508.
ACCESSION I67718
VERSION I67718.1 GI:2731253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1420)
AUTHORS Gyuris J., Lamphere L. and Beach D.
TITLE Inhibitors of cell-cycle progression, and uses related thereto
JOURNAL Patent: US 5672508-A 1 30-SEP-1997;
FEATURES
    Location/Qualifiers
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            1..1420
            /organism="unknown"
BASE COUNT 322 a 410 c 458 g 230 t
ORIGIN
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alignment_scores:
    Quality: 785.00      Length: 156
    Ratio: 5.065         Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718
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alignment_block:

US-09-016-869A-2 x I67718 ..

Align seg 1/1 to: I67718 from: 1 to: 1420

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17 aThraAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34
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759 CACGCCCGCGCGCGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGG 808
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34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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809 CGGTGGCGCTGCCCAACGACCGATAGTTACGGTCGGAGCGCATCCAG 858
|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
|||||
859 GTCATGATGATGGGCGCGCGAGTGGCGAGCTGCTGCTCCACGG 908
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
909 CGCGAGCGCCAACTGCGCGGACCGCGCCACTCTCACCGACCGGTGCACG 958
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84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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959 ACGTGCGCGGGAGGGCTTCTTGACACGCTGGTGTGCTGCACCGGGCC 1008
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
1009 GGGCGCGCTGGACGTGCGGATGCTGGGGCGCTGCTGCCCGTGGACCT 1058
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117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
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1059 GCTGAGGAGCTGGGCCATTCGCGTGTGCGACGCTGGTGTGCTGCACGGCGTG 1108
|||||
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
|||||
1109 CGGGGGCACCAGAGGCGATACCATGCCGATAGATGCCGCGGAAGGT 1158
|||||
151 ProSerAspIleProAsp 156
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1159 CCTCAGACATCCCGAT 1176
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seq_name: gb_pr4:AF115544

seq_documentation_block: 793 bp mRNA PRI 01-FEB-1999
LOCUS AF115544
DEFINITION Homo sapiens cyclin-dependent kinase inhibitor p12 (p16INK4a) mRNA,
alternatively spliced form, complete cds.
ACCESSION AF115544
VERSION AF115544.1 GI:4206166
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 793)
AUTHORS Robertson K.D. and Jones, P.A.
TITLE Tissue-specific alternative splicing in the human INK4a/ARF cell
cycle regulatory locus
JOURNAL Oncogene (1998) In press
REFERENCE 2 (bases 1 to 793)
AUTHORS Robertson K.D. and Jones, P.A.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1998) Cancer Center, University of Southern
California, 1441 Eastlake Ave. MS 73, Los Angeles, CA 90033, USA
FEATURES
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        /map="p"
        /tissue_type="pancreas"
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        1..351
        /gene="p16INK4a"
        /note="alternatively spliced form of p16INK4a"
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        /product="cyclin-dependent kinase inhibitor p12"
        /protein_id="AAD11437.1"
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/db_xref="GI:4206167"
/translation="MEPRAGSSMEPSADWLATAAARGVEEVYRALLEAGALPNAPNSY
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PDALGAWETKEE"
BASE COUNT 153 a 213 c 300 g 127 t
ORIGIN

alignment_scores:
Quality: 716.50 Length: 248
Ratio: 4.623 Gaps: 2
Percent Similarity: 62.500 Percent Identity: 61.694
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1 ATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
17 aThrAlaAlaAlaArgGlyArgValGluGluValAlaArgAlaLeuGluA 34
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51 CACGGCGCGCGCGGGGTCTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIle.G1 50
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101 CGGGGGCGCTGCCACGCCACCAAGTAATGTTACGGTCGGAGCGCATCCAG 150
50 n..... 50
151 GTGGGTAGAAGGCTTCGACGGGAGCAGGGGATGGCGGGGACTCTCGAG 200
50 50
201 GACGAAGTTTCAGGGAATGGAAATCAGTACGGCTTCGATCTCCGGA 250
50 50
251 AAAAGGGAGGCTTCCTGGGAGTTTTCAGAAGGGTTTGTATATACAGA 300
50 50
301 CCTCTCTCGGACGCCCTGGGGGCTTGGGAACCAAGGAAGGAATG 350
50 50
351 AGGAGCCACCGCGGTACAGATCTCTCGAATGCTGAGAGATCTGAAGGG 400
51ValMetMetMetGlySerAlaArgVa 59
401 GGAACATATTGTTATTAGATGGAAGTCATGATGGCGCAGCGCCGTGT 450
59 laAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProA 76
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451 GGGGAGCTGCTGCTGCTCCACGGCGGGAGCCCACTGGCGCCGCCCG 500
76 laThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAsp 92
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501 CCACCTCTACCCGACCGCTGCACAGCAGCTGCCCGGAGGGCTTCCTGGAC 550
93 ThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAl 109
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551 ACGCTGGTGTGCTGCACCGCGCGGGCGCGGCTGGACGTGCGCATGC 600
109 aTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisArgAspV 126
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601 CTGGGGCGCTGTGCGGTGGACCTGGCTGGAGAGCTGGGGCATCGCGATG 650
126 alAlaArgTyrLeuArgAlaAlaGlyThrArgGlySerAsnHis 142
|||||||||||||||||||||||||||||||||||||||||||||
651 TGCACGGTACCTCGCGCGGCTCGGGGGGCCACCGAGGCGAGTAACCAT 700

143 AlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
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701 GCCCGCATAGATCCCGGAAGTCCCTCAGACATCCCGCAT 742
seq_name: gb_pr2:HSU26727
seq_documentation_block:
LOCUS HSU26727 1017 bp mRNA PRI 30-NOV-1995
DEFINITION Human p16INK4/MTS1 mRNA, complete cds.
ACCESSION U26727
VERSION U26727.1 GI:862412
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1017)
AUTHORS Duro,D., Bernard,O., Della Valle,V., Berger,R. and Larsen,C.J.
TITLE A new type of p16INK4/MTS1 gene transcript expressed in B-cell malignancies
JOURNAL Oncogene 11 (1), 21-29 (1995)
MEDLINE 95349933
REFERENCE 2 (bases 1 to 1017)
AUTHORS Larsen,C.-J.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-1995) Christian-Jacques Larsen, Institut de Genetique moleculaire, U-301 Inserm, 27, rue Juliette Dodu, Paris 75010, France
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="13 RPMI 8226"
/chromosome="9"
/map="9p21"
/cell_line="RPMI 8226"
/cell_type="lymphoid"
/tissue_type="hematopoietic"
1..220
/gene="p16INK4/MTS1"
/note="also called exon 0.18, substituted by alternative splicing to p16INK4 exon 1"
number=1
1..1017
/gene="p16INK4/MTS1"
28..426
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/note="a frameshift between exon 1 (0.18) and exon 2 changed the ORF of p16INK4 gene."
/codon_start=1
/protein_id="AA82236.1"
/db_xref="GI:862413"
/translation="MVRFLVTLIRACGPRVRVVFVHIPRLTGEWAAPGAPAAVA
LYMLLSQRQLGQPLPRPGHDDGQRPSGGGAAAPRRGAQLRRPRHSHPTARRCPG
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221..527
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number=2
528..1017
/gene="p16INK4/MTS1"
number=3
BASE COUNT 215 a 297 c 291 g 214 t
ORIGIN
alignment_scores:
Quality: 553.50 Length: 174
Ratio: 4.358 Gaps: 2
Percent Similarity: 72.989 Percent Identity: 66.092
alignment_block:
US-09-016-869A-2 x HSU26727 ..

DEFINITION Sequence 13 from patent US 5739027.
ACCESSION AR001325
VERSION AR001325.1 GI:3963392
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1131)
TITLE MTS1E1.beta. gene
JOURNAL Patent: US 5739027-A 13 14-APR-1998;
FEATURES Location/Qualifiers
1..1131
Source

BASE COUNT 232 a 327 c 343 g 229 t
ORIGIN

alignment_scores:
Quality: 553.00 Length: 107
Ratio: 5.168 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-016-869A-2 x AR001325 ..

Align seg 1/1 to: AR001325 from: 1 to: 1131

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50 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuH1 66
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332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
382 CGGCGCGAGCGCAACTGCGCGCAGCCGCCACTCTCACCCGACCCGTC 431
83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
|||||
432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116
|||||
482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAla 133
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532 CCTGGCTGAGGAGCTGGGCCATCGCATGCGCACGGTACCTGCGCGCGG 581
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
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582 CTGCGGGGGGACCCAGAGGAGTAAACCATGCCCGCATAGATGCCCGGAA 631
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seq_name: gb_pat:AR037505

seq_documentation_block:

LOCUS AR037505 1131 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5801236.
ACCESSION AR037505
VERSION AR037505.1 GI:5955361
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1131)

AUTHORS
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 13 01-SEP-1998;
FEATURES Location/Qualifiers
1..1131
source

BASE COUNT 232 a 327 c 343 g 229 t
ORIGIN

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alignment_scores:
Quality: 553.00 Length: 107
Ratio: 5.168 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-016-869A-2 x AR037505 ..

Align seg 1/1 to: AR037505 from: 1 to: 1131

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332 CAGGTCATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCA 381
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
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382 CGGCGCGAGCGCAACTGCGCGCAGCCGCCACTCTCACCCGACCCGTC 431
83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
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432 ACGACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGGTCTGCACCGG 481
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116
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482 GCCGGGCGCGGCTGGAGCTGCGCGATGCTGGGCGCTGCTGCCCGTGA 531
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAla 133
|||||
532 CCTGGCTGAGGAGCTGGGCCATCGCATGCGCACGGTACCTGCGCGCGG 581
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
|||||
582 CTGCGGGGGGACCCAGAGGAGTAAACCATGCCCGCATAGATGCCCGGAA 631
150 GlyProSerAspIleProAsp 156
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632 GGTCCCTCAGACATCCCGAT 652
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OM of: US-09-016-869A-2 to: N_Geneseq_36:* out_format : pfs

Date: Jul 21, 2000 9:30 AM

About: Results were produced by the GenCore software, version 4.5,

Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.500 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -MINMATCH=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
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Search information block:

Query: US-09-016-869A-2

Query length: 156

Database: N_Geneseq_36:*

Database sequences: 311585

Database length: 125096042

Search time (sec): 109.050000

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N_Geneseq_36:T00747	+	796.00	1342.73	3.4e-67	947	Multiple tumour suppressor 1 (M
N_Geneseq_36:V11238	+	789.00	1337.06	7.1e-67	471	Human MTS1 cDNA. DNA specific
N_Geneseq_36:V53819	+	789.00	1337.06	7.1e-67	471	Nucleotide sequence of the CDS
N_Geneseq_36:V70583	+	789.00	1337.06	7.1e-67	471	cDNA encoding a human multiple
N_Geneseq_36:T72311	+	789.00	1330.84	1.6e-66	947	Human multiple tumour suppressor
N_Geneseq_36:V11270	+	789.00	1330.84	1.6e-66	947	Human MTS1 cDNA variant. DNA sp
N_Geneseq_36:V53851	+	789.00	1330.84	1.6e-66	947	Coding sequence 3 of the multi
N_Geneseq_36:T60915	+	789.00	1330.84	1.6e-66	947	cDNA encoding a human multiple
N_Geneseq_36:T60951	+	789.00	1330.47	1.7e-66	987	Tumour suppressor p16 coding se
N_Geneseq_36:X26233	+	788.00	1331.38	1.5e-66	737	Truncated p27/p16 fusion protei
N_Geneseq_36:X26234	+	788.00	1331.38	1.5e-66	737	Truncated p27/p16 fusion protei
N_Geneseq_36:X26231	+	788.00	1328.42	2.2e-66	1028	Truncated p27/p16 fusion prote
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N_Geneseq_36:T74053	+	788.00	1327.83	2.3e-66	1098	CDK inhibitory fusion protein
N_Geneseq_36:X26224	+	788.00	1327.83	2.3e-66	1098	Human p16p27 fusion protein en
N_Geneseq_36:X26225	+	788.00	1327.64	2.4e-66	1121	Human p16p27 fusion protein en
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N_Geneseq_36:X26223	+	788.00	1327.47	2.4e-66	1143	Human p16(GS)p27 fusion protei
N_Geneseq_36:T74051	+	785.00	1320.45	6.0e-66	1420	CDK inhibitory fusion protein
N_Geneseq_36:X26220	+	785.00	1320.45	6.0e-66	1420	Human p27-p16 fusion protein e
N_Geneseq_36:T69768	+	782.00	1325.18	3.3e-66	471	Human multiple tumour suppress
N_Geneseq_36:T69769	+	781.00	1323.48	4.1e-66	471	Human multiple tumour suppress
N_Geneseq_36:T69791	+	787.00	1293.49	1.9e-64	948	Inhibitor of cyclin dependent
N_Geneseq_36:T00736	+	760.00	1288.30	3.7e-64	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:Q99158	+	760.00	1288.30	3.7e-64	447	Human multiple tumour suppress
N_Geneseq_36:T00749	+	753.00	1276.42	1.7e-63	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:T00750	+	752.00	1274.72	2.1e-63	447	Multiple tumour suppressor 1 (M
N_Geneseq_36:T00744	+	533.00	928.66	4.0e-44	1131	Multiple tumour suppressor 1 e
N_Geneseq_36:Q99164	+	533.00	928.66	4.0e-44	1131	Human MTS polypeptide, MTS1 e
N_Geneseq_36:T69780	+	533.00	928.66	4.0e-44	1131	Human multiple tumour suppress
N_Geneseq_36:V11249	+	533.00	928.66	4.0e-44	1131	Human MTS1-beta cDNA. DNA sp
N_Geneseq_36:V53830	+	533.00	928.66	4.0e-44	1131	Coding sequence 1 of the multi
N_Geneseq_36:T69594	+	533.00	928.66	4.0e-44	1131	cDNA encoding a human multiple
N_Geneseq_36:T02964	+	533.00	900.66	1.4e-42	580	Cell-cycle regulatory protein p
N_Geneseq_36:T00739	+	530.00	889.19	6.3e-42	1187	Multiple tumour suppressor 1 (M
N_Geneseq_36:V11240	+	530.00	889.19	6.3e-42	1187	Human MTS1 genomic DNA includi
N_Geneseq_36:V53821	+	530.00	889.19	6.3e-42	1187	Coding sequence 2 of the multi
N_Geneseq_36:T69585	+	530.00	889.19	6.3e-42	1187	Human multiple tumour suppress
N_Geneseq_36:V70624	+	529.00	897.33	2.2e-42	393	Mouse multiple tumour suppress
N_Geneseq_36:T00745	+	526.00	886.48	8.9e-42	751	Multiple tumour suppressor 2 (M

N_Geneseq_36:Q99165	+	526.00	886.48	8.9e-42	751	Human multiple tumour suppressor
N_Geneseq_36:T69781	+	526.00	886.48	8.9e-42	751	Human multiple tumour suppressor
N_Geneseq_36:V11250	+	526.00	886.48	8.9e-42	751	Human MTS2 cDNA. DNA specific
N_Geneseq_36:V53831	+	526.00	886.48	8.9e-42	751	Coding sequence 2 of the mul
seq_name: N_Geneseq_36:T02962						
seq_documentation_block:						
ID T02962 standard; cDNA; 994 BP.						
AC T02962;						
DT 01-MAR-1996 (first entry)						
DE Cell-cycle regulatory protein p16 cDNA.						
KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;						
KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;						
ss; ds.						
OS Homo sapiens.						
FH Key						
FT cds						
FT						
PN W09528483-A1.						
PD 26-OCT-1995.						
PF 14-APR-1995; U04636.						
PR 14-APR-1994; US-227371.						
PR 25-MAY-1994; US-248812.						
PR 14-SEP-1994; US-306511.						
PR 29-NOV-1994; US-346147.						
PA (COLD-) COLD SPRING HARBOR LAB.						
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;						
DR WPI: 95-373798/48.						
DR P-PSDB: R85116.						
PT New cell cycle regulating proteins bind to cyclin dependent kinase -						
PT and related nucleic acids, antibodies etc., used in diagnosis and						
PT therapy of abnormal cell proliferation, degeneration etc.						
PS Claim 43; Page 76-77; 109pp; English.						
CC cDNA (T02962) coding for the human cell-cycle regulatory (CCR)						
CC protein p16 (R85116) was isolated using a 2-hybrid screening assay						
CC in Saccharomyces cerevisiae. The p16 gene was mapped to chromosome						
CC 9p21-22. The isolated cDNA can be used: to detect mutations in						
CC CCR genes that lead to cell proliferation; to breed transgenic						
CC animals to study cellular disorders involving CCR allele						
CC mutation/misexpression; and to correct CCR-deficient cells						
CC (gene therapy).						
SQ Sequence 994 BP; 225 A; 279 C; 293 G; 197 T;						
alignment_scores:						
Quality: 800.00						
Ratio: 5.128						
Percent Similarity: 100.000						
Gaps: 0						
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alignment_block:						
US-09-016-869A-2 x T02962						
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41 ATGATGATCGCGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGC 90						
17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34						
91 CACGGCGCGCGCGCGGGTCCGGTAGAGGAGGTCCGGCGCTGCTGGAGG 140						
34 laValAlaLeuProAsnAlaProAsnSerTyrglyArgArgProIleGln 50						
141 CGGTGGCGCTGCCAACGACGACCATGATAGTACGTCGGAGCGCGATCCAG 190						
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67						
191 GTCATGATGATGATGCGCGCGCGCGGAGTGGCGAGTCTGCTGCTCCACGG 240						
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84						

PT mutation(s) and their treatment

PS Disclosure: Column 61-62: 72bp; English.
CC This cDNA sequence encodes a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

alignment_scores:
Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V11238 ..

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|||||
17 aThrAlaAlaAArgGlyArgValGluGluValAlaArgAlaLeuGluA 34
|||||
51 CACGGCGCGCGCGGGTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100
|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCAACGACGACCAATAGTACGGTCGGAGCGCATCCAG 150
|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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151 GTCATGATGATGGCAGCGCGCGGAGTGGCGGAGCTGCTGTCTCCACG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84
|||||
201 CGGGAGCGCAACTGCGCGCAGCCGCGCACTCTCACCCGACCGCTGCACG 250
|||||
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGCGCGGGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGG 300
|||||
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGGCTGGACGTGCGGATGCTGGGCGCTGCTGGCGGTGGACCT 350
|||||
117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
|||||
351 GGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACCTGCGCGCGCTG 400
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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401 CGGGGGCCAGCAGGAGGAGTAAACATCCCGCATAGATGCCGCGGAAGT 450
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151 ProSerAspIleProAsp 156
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451 CCCTCAGACATCCCGAT 468
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seq_name: N_Geneseq_36.V53819

seq_documentation_block:

ID V53819 standard; CDNA; 471 BP.

AC V53819;

DT 04-DEC-1998 (first entry)

DE Nucleotide sequence of the CDS of the multiple tumour suppressor 1.

KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.

OS Homo sapiens.

FA Key Location/Qualifiers

CDS 1..471
/*tag= a
/product= "human MTS-1"

US5801236-A.
01-SEP-1998.
07-JUN-1995; 480810.
07-JUN-1995; US-480810.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-U03316.
(MYRI-) MYRIAD GENETICS INC.
Kamb A;
WPI: 98-494842/42.
P-PSDB: W74549.
Nucleic acids based on multiple tumour suppressor, MTS, sequences -
useful as hybridisation probes, primers and recombinant production
of MTS in the diagnosis and treatment of cancers related to MTS
mutation(s)
PS Claim 1: Column 61-62: 73bp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor 1
(MTS-1) gene, used in the method of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer, e.g. by
standard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein mimetics, also for therapeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
itself may also be used to restore MTS function in a cell.
SQ Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

alignment_scores:

Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V53819 ..

Align seg 1/1 to: V53819 from: 1 to: 471

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1 ATGGAGCGCGCGGGGAGCAGCATGAGCCTTCGGCTGACTGGCTGGC 50
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17 aThrAlaAlaAArgGlyArgValGluGluValAlaArgAlaLeuGluA 34
|||||
51 CACGGCGCGCGCGGGTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100
|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCAACGACGACCAATAGTACGGTCGGAGCGCATCCAG 150
|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
|||||
151 GTCATGATGATGGCAGCGCGCGGAGTGGCGGAGCTGCTGTCTCCACG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84
|||||
201 CGGGAGCGCAACTGCGCGCAGCCGCGCACTCTCACCCGACCGCTGCACG 250
|||||
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
|||||
251 ACGTGCGCGGGAGGGCTTCCTGGACACGCTGGTGGTGGTGGTGGTGG 300
|||||
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
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301 GGGGGCGGCTGGACGTCGGCGCATCCCTGGGGCCCTCTGCGCGTGGACCT 350
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
 351 GGCTGAGGAGCTGGCCATCGCGATGTCGACGGTACCTGCGCGGGCTG 400
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
 401 CGGGGGGACCAAGAGCGATACCATGCCCGCATAGATGCCGCGGAAGT 450
 151 ProSerAspIleProAsp 156
 451 CCTCAGACATCCCCGAT 468

seq_name: N_Geneseq_36:V70583

seq_documentation_block:

ID V70583 standard; cDNA; 471 BP.
 AC V70583;
 DT 03-FEB-1999 (first entry)
 DE cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..471
 FT misc_feature 150..151
 FT misc_feature 478..458
 FT note="splice site"
 FT note="splice site"
 FT US5843756-A.
 PN 01-DEC-1998.
 PD 28-JUL-1995; 058735.
 PF 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI; 99-044585/04.
 DR P-PSDB; W80524.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design
 PS Disclosure: Columns 63-66; 80pp; English.
 CC The present sequence encodes a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
 CC Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;
 SQ

alignment_scores:
 Quality: 789.00 Length: 156
 Ratio: 5.090 Gaps: 0
 Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V70583 ..
 Align seg 1/1 to: V70583 from: 1 to: 471

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 1 ATGAGCGCGCGCGGAGCAGCAGTGGAGCCCTTCGGCTGACTGGCTGC 50
 17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
 51 CACGCCCGCGCGCGGTGCGGTAGAGGAGTGGCGGCTGCTGGAGG 100
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgProIleGln 50

117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
 351 GGCTGAGGAGCTGGCCATCGCGATGTCGACGGTACCTGCGCGGGCTG 400
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
 401 CGGGGGGACCAAGAGCGATACCATGCCCGCATAGATGCCGCGGAAGT 450
 151 ProSerAspIleProAsp 156
 451 CCTCAGACATCCCCGAT 468
 seq_name: N_Geneseq_36:T72311
 seq_documentation_block:
 ID T72311 standard; cDNA; 947 BP.
 AC T72311;
 DT 10-SEP-1997 (first entry)
 DE Human multiple tumour suppressor gene 1.
 KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..471
 FT US5624819-A.
 PN 29-APR-1997.
 PD 18-MAR-1994; 214582.
 PF 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03537.
 PR 07-JUN-1995; US-474177.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 PI WPI; 97-258217/23.
 DR P-PSDB; W19251.
 PT Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
 PS Claim 1; Columns 87-90; 72pp; English.
 CC The present sequence the human multiple tumour suppressor gene 1 (MTS1), useful in cancer diagnosis.
 CC Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;
 SQ

alignment_scores:
 Quality: 789.00 Length: 156
 Ratio: 5.090 Gaps: 0
 Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:
 US-09-016-869A-2 x T72311 ..

Align seg 1/1 to: T72311 from: 1 to: 947

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17 aThAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluA 34
|||||
51 CACGGCGCGCGCGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAGG 100
|||||
34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
|||||
101 CGGGGGCGCTGCCCAACGACCGCAATAGTTACGGTCGGAGCCGATCCAG 150
|||||
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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151 GTCATGATGATGGCAGCGCGGAGTGGCGAGCTGCTGCTGCCACGG 200
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67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
201 CGCGAGCGCCAACTGCCCGGACCGCCGCACTCTCACCGGACCGCTGCACG 250
|||||
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 ACGTGTCCCGGGAGGGTCTCTGGACACGCTGGTGGTCTGCACCGGGCC 300
|||||
101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
|||||
301 GGGCGCGGCTGGACGTGCGGATGCTGGGGCGCTCTGCCCGTGGACCT 350
|||||
117 uAlaGluLeuLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
|||||
351 GGCTGAGGAGCTGGGGCATCGCATGTGCGACGCTAGCTGCGCGCGCTG 400
|||||
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
|||||
401 CGGGGGCACAGAGGAGGATACCATGCCCGCATAGATGCCCGCGGAGGT 450
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151 ProSerAspIleProAsp 156
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451 CCCTCAGACATCCCGAT 468
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seq_name: N_Geneseq_36.V11270

seq_documentation_block:

ID V11270 standard; cDNA; 947 BP.
AC V11270;
DT 15-JUL-1998 (first entry)
DE Human MTS1 cDNA variant.
KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition; ds.
OS Homo sapiens.

FH Key Location/Qualifiers

FT misc_feature 151

FT /tag- a

FT /note- "splice site acceptor"

FT misc_feature 458

FT /tag- b

FT /note- "splice site acceptor"

FN US5739027-A.

PD 14-APR-1998.

PF 07-JUN-1995; 487033.

PR 07-JUN-1995; US-487033.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-250421/22.

PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment

PS This cDNA sequence encodes a variant of the human multiple tumour

CC suppression protein, MTS1. The MTS gene locus is also referred to as the

CC familial melanoma (MLM) gene locus, located on human chromosome 9p21.

CC germ line mutations in MTS genes can be used in the diagnosis of

CC predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma,

CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of

CC the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach

CC and rectum

SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment_scores:

Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0

Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V11270 ..

Align seg 1/1 to: V11270 from: 1 to: 947

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17

||||:|||||

1 ATGGAGCGCGCGGGAGGAGCAGCATGGAGCTTCGGCTGACTGCTGGCTGGC 50

|||||

17 aThAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluA 34

|||||

51 CACGGCGCGCGGGTGGGTAGAGAGGTGCGGCGCTGCTGGAGG 100

|||||

34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50

|||||

101 CGGGGGCGCTGCCCAACGACCGCAATAGTTACGGTCGGAGGCCGATCCAG 150

|||||

51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67

|||||

151 GTCATGATGATGGCGACGCGCGGAGTGGCGAGCTGCTGCTGCCACGG 200

|||||

67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84

|||||

201 CGCGAGCGCCAACTGCCCGGACCGCCGCACTCTCACCGGACCGCTGCACG 250

|||||

84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100

|||||

251 ACGTGTCCCGGGAGGGTCTCTGGACACGCTGGTGGTCTGCACCGGGCC 300

|||||

101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117

|||||

301 GGGCGCGGCTGGAGCTGCGGATGCTGGGGCGCTGCTGCCCGTGGACCT 350

|||||

117 uAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134

|||||

351 GGCTGAGGAGCTGGGGCATCGCATGTGCGACGCTAGCTGCGCGCGCTG 400

|||||

134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150

|||||

401 CGGGGGCACAGAGGAGGATACCATGCCCGCATAGATGCCCGCGGAGGT 450

|||||

151 ProSerAspIleProAsp 156

|||||

451 CCCTCAGACATCCCGAT 468

seq_name: N_Geneseq_36.V53851

seq_documentation_block:

ID V53851 standard; cDNA; 947 BP.

AC V53851;

DT 04-DEC-1998 (first entry)

DE Coding sequence 3 of the multiple tumour suppressor 1.

KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PF 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 98-494842/42.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 useful as hybridisation probes, primers and recombinant production
 of MTS in the diagnosis and treatment of cancers related to MTS
 mutation(s)
 PT Claim 1; Fig 17; 73pp; English.
 PS This is the nucleotide sequence of the multiple tumour suppressor 1
 CC (MTS-1) gene, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations
 CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.
 SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment_scores:
 Quality: 789.00 Length: 156
 Ratio: 5.090 Gaps: 0
 Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V53851 ..

Align seg 1/1 to: V53851 from: 1 to: 947

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
 1 ATGGAGCGCGCGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
 17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
 51 CACGGCGCGCGCGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
 101 CGGGGGCGCTGCCACACCGACCATAGTACGGTCGGAGCGCGATCCAG 150
 51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
 151 GTCATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
 201 CGCGGAGCCCAACTGCGCGAGCCCGCCCACTCTCACCCGACCGGTGCG 250
 84 sPalAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
 251 AGCTGCCCCGGAGGGCTTCCTGGACACCCCTGGTGTGCTGCCCGGGCC 300
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
 301 GGGCGCGCGCTGAGTGGCGCATGCTGCGGGCCGCTCTGCCCGTGGACCT 350

117 uAlaGluLeuLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
 351 GGCTGAGGAGCTGGCCCATCGCATGTGCGACGGTACCTGCGCGCGGTG 400
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
 401 CGGGGGCGCAGAGGCGCATACCATGCCCATAGATGCCCGCGGAAGGT 450
 151 ProSerAspIleProAsp 156
 451 CCTTCAGACATCCCGCAT 468

seq_name: N_Geneseq_36.V70615

seq_documentation_block:

ID V70615 standard; cDNA; 947 BP.

AC V70615;

DT 03-FEB-1999 (first entry)

DE cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.

KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT misc_feature 151

FT /tag= a /note= "splice site acceptor"

FT /tag= b

FT /note= "splice site acceptor"

FT misc_feature 458

FT /tag= b

FT /note= "splice site acceptor"

PN US5843756-A.

PD 01-DEC-1998.

PF 28-JUL-1995; 058735

PR 28-JUL-1995; US-508735.

PR 07-JUN-1995; US-487033.

PA (MYRI-) MYRIAD GENETICS INC.

PI Jiang P, Kamb A, Stone S;

DR WPI; 99-044585/04.

PT Mouse multiple tumour suppressor gene segment - useful for primer

PT design

PS Disclosure; Fig 17; 80pp; English.

CC The present sequence represents the cDNA sequence for a human multiple

CC tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene

CC can be used to design primers to detect abnormalities i.e. polymorphisms

CC which may predispose towards malignancies such as melanoma, leukaemia,

CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,

CC thyroid, pancreas, uterus and kidneys.

CC Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

alignment_scores:

Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0

Percent Similarity: 99.359 Percent Identity: 98.718

alignment_block:

US-09-016-869A-2 x V70615 ..

Align seg 1/1 to: V70615 from: 1 to: 947

1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
 1 ATGGAGCGCGCGCGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGC 50
 17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluA 34
 51 CACGGCGCGCGCGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
 101 CGGGGGCGCTGCCCAACCGACCATAGTACGGTCGGAGCGCGATCCAG 150
 51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
 151 GTCATGATGATGGCAGCGCCCGAGTGGCGGAGCTGCTGCTCCACGG 200

67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisa 84
 201 CGGGAGCCCACTGGCGGACACCCGCACTCTCACCCGACCGGTGCACG 250
 84 sPalaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisaArgAla 100
 251 ACCTGCCCGGGAGGCTCTCTGCACACGCTGGTGTGTGCACCGGGCC 300
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
 301 GGGCGCGCTGCACGCTGCGCGATGCTGGGCGCTCTGCGCGGTGACCT 350
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
 351 GGTGAGGAGCTGGGCGATGCGCATGCGCATGCGCATGCGCGCGGCTG 400
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
 401 CGGGGGCCACGAGCGATACCATGCGCGCATAGATGCGCGCGGAGGT 450
 151 ProSerAspIleProAsp 156
 451 CCCTCAGACATCCCGAT 468

seq_name: N_Geneseq_36:T60951

seq_documentation_block:
 ID T60951 standard; DNA; 987 BP.
 AC T60951;
 DT 28-OCT-1997 (first entry)
 DE Tumour suppressor p16 coding sequence.
 KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;
 KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;
 KW anti-angiogenic activity; hyperproliferative disorder; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 41..511
 FT /*tag= a
 FT /product= Tumour suppressor p16
 FT
 PN WO9703635-A2.
 PD 06-FEB-1997.
 PF 17-JUL-1996; U11787.
 PR 17-JUL-1995; US-502881.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PI Jin X, Roth J;
 DR WPI; 97-132336/12.
 DR P-PSDB; W10627.
 PT Expression construct contg. DNA for tumour suppressor p16 - to
 PT restore p16 activity to transformed cells, useful for treating lung
 PT or bladder cancer or melanoma
 PS Disclosure; Fig 1a; 92pp; English.
 CC This sequence represents the coding sequence for the tumour suppressor
 CC p16. This sequence is joined to a promoter functional in eukaryotic cells
 CC and used in the expression construct of the invention. p16 is an
 CC inhibitory subunit, which is involved in the control of cyclin-dependent
 CC kinase 4 activity, and functions as a tumour suppressor. By detecting
 CC this sequence or the encoded protein, cancer cells can be detected. When
 CC the nucleic acid molecule is in the sense orientation, the expression
 CC construct can be used to restore p16 function in a cell, particularly by
 CC reversing the transformed phenotype in tumours, especially lung or
 CC bladder cancer or melanoma. It may also have anti-angiogenic activity,
 CC and inhibit hyperproliferative disorders, e.g. restenosis. When the
 CC nucleic acid molecule is inserted in the antisense orientation, the
 CC expression construct inhibits p16 function. Reduced or increased levels
 CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by
 CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
 CC or immunoassay.
 SQ Sequence 987 BP; 219 A; 279 C; 295 G; 194 T;

alignment_scores:
 Quality: 789.00 Length: 156

Ratio: 5.090 Gaps: 0
 Percent Similarity: 99.359 Percent Identity: 98.718
 alignment_block:
 US-09-016-869A-2 x T60951 ..
 Align seg 1/1 to: T60951 from: 1 to: 987
 1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
 41 ATGGAGCCGGCGGGGAGCAGCATGGAGCCCTTCGGCTGACTGCTGGC 90
 17 aThrAlaAlaAlaArgGlyArgValGluGluValAlaAlaLeuLeuGluA 34
 91 CACGGCCGGCGGGCGGGGTGGGTAGAGAGGTGGCGGCGCTGCTGGAGG 140
 34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
 141 CGGGGGCGCTGCCCAACACCGCAATAGTTACGGTCGGAGCGCGATCCAG 190
 51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisaG 67
 191 GTCATGATGATGGCAGCGCCGAGTGCGGAGCTGCTGCTGCTCCACGG 240
 67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisa 84
 241 CGCGGAGCCCACTGCGCGGACCCCGCACTCTCACCCGACCGGTGCACG 290
 84 sPalaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisaArgAla 100
 291 ACCTGCCCGGGAGGCTCTCTGCACACGCTGGTGTGTGCACCGGGCC 340
 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
 341 GGGCGCGGCTGCACGCTGCGCGATGCTGGGCGCTCTGCGCGGTGACCT 390
 117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAla 134
 391 GGCTGAGGAGCTGGGCGATGCGCATGCGCATGCGCATGCGCGCGGCTG 440
 134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
 441 CGGGGGCCACGAGCGAGTACCATGCGCGCATAGATGCGCGCGGAGGT 490
 151 ProSerAspIleProAsp 156
 491 CCCTCAGACATCCCGAT 508

seq_name: N_Geneseq_36:X26233

seq_documentation_block:
 ID X26233 standard; DNA; 737 BP.
 AC X26233;
 DT 25-MAY-1999 (first entry)
 DE Truncated p27/p16 fusion protein encoding DNA.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerosis; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16; truncated; ss.
 OS Homo sapiens.
 PN WO9906540-A2.
 PD 11-FEB-1999.
 PF 29-JUL-1998; U15759.
 PR 29-JUL-1997; US-902572.
 PA (MITO-) MITOPIX INC.
 PI Beach DH, Gyuris J, Lamphere L;
 DR WPI; 99-153770/13.
 DR P-PSDB; W95105.
 PT Fusion and chimeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and

PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 PS Claim 60; Page 84-85; 88pp; English.
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for
 CC detailed uses of the recombinant transfection system. The present
 CC sequence represents a DNA encoding a human truncated p27/p16 fusion
 CC protein.
 SQ Sequence 737 BP; 135 A; 227 C; 267 G; 108 T;

alignment_scores:
 Quality: 788.00 Length: 155
 Ratio: 5.117 Gaps: 0
 Percent Similarity: 99.355 Percent Identity: 99.355
 alignment_block:
 US-09-016-869A-2 x X26233 ..

Align seg 1/1 to: X26233 from: 1 to: 737

2 AspProAlaAlaGlySerMetGluProSerAlaAspTrpLeuAla18
 262 GATCGCGCGGGGAGCAGCATGGAGCTTCGGCTGACTGCTGCCAC 311
 18 rAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluAla1av 35
 312 GCGCGCGCGCGGGTTCGGGTAGAGAGGTGCGGCGCTGCTGGAGCGG 361
 35 AlAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
 362 GGGCGCTGCCCAACGACCGATAGTACGTCGGAGGCCGATCCAGGTC 411
 52 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68
 412 ATGATGATGGCAGCGCCGAGTGGCGAGGTGCTGCTCCACGCGGC 461
 68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
 462 GGAGCCCACTCGCGCGACCCCGCCACTCTCACCGACCCGTCGACGAG 511
 85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
 512 CTGCGCGGGAGGGCTTCTGGACAGCTGGTGGTGGTGGTGGTGGTGG 561
 102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
 562 GCGCGCTGGAGCTGCGCGATGCCCTGGGCGCTCTGCCGTGGACCTGCG 611
 118 aGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaAlaG 135
 612 TGAGAGCTGGGCCATCGCGATGTCGACGAGTACCTGCGCGCGGTGCGG 661
 135 lYGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyPro 151
 662 GGGGACACAGAGGAGTAAACATGCCCCGATAGTCCCGGAGAGTGCC 711
 152 SerAspIleProAsp 156
 712 TCAGACATCCCGAT 726

seq_name: N_Geneseq_36.X26234

seq_documentation_block:

ID X26234 standard; DNA; 782 BP.
 AC X26234;
 DT 25-MAY-1999 (first entry)
 DE Truncated p27/p16 fusion protein encoding DNA.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 KW tachycardia; human; p27; p16; truncated; ss.
 OS Homo sapiens.
 PN WO9006540-A2.
 PD 11-FEB-1999.
 PF 28-JUL-1998; U15759.
 PR 29-JUL-1997; US-902572.
 PA (MITO-) MITOTIX INC.
 DR PI Beach DH, Gyuris J, Lamphere L;
 DR P-PSDB; W95106.
 PT Fusion and chimaeric proteins including cyclin-dependent kinase
 PT binding motif - used for regulation of cell proliferation and
 PT differentiation, for treatment of, e.g. vascular injury, cancers,
 PT fibrosis and neurodegeneration
 PS Claim 60; Page 85; 88pp; English.
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 CC transfection system (A) that comprises: (i) first gene construct
 CC comprising a sequence encoding an inhibitory polypeptide containing at
 CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
 CC linked to a transcription regulator functional in eukaryotic cells; (ii)
 CC second gene construct comprising a sequence encoding a polypeptide that
 CC promotes endothelialisation, and (iii) a gene delivery composition for
 CC delivering the GCs to a cell for transfection. Also provided are nucleic
 CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
 CC polypeptide sequence (TP) from an intracellular protein that alters a
 CC cellular process when FP enters the cell, and (ii) a transcellular
 CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 CC consists of at least one CDK-binding motif and a TCP. See X26220 for
 CC detailed uses of the recombinant transfection system. The present
 CC sequence represents a DNA encoding a human truncated p27/p16 fusion
 CC protein.
 SQ Sequence 782 BP; 137 A; 236 C; 295 G; 114 T;

alignment_scores:

Quality: 788.00 Length: 155
 Ratio: 5.117 Gaps: 0
 Percent Similarity: 99.355 Percent Identity: 99.355

alignment_block:

US-09-016-869A-2 x X26234 ..

Align seg 1/1 to: X26234 from: 1 to: 782

2 AspProAlaAlaGlySerMetGluProSerAlaAspTrpLeuAla18
 307 GATCGCGCGGGGAGCAGCATGGAGCTTCGGCTGACTGCTGCCAC 356
 18 rAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluAla1av 35
 357 GCGCGCGCGCGGGTTCGGGTAGAGAGGTGCGGCGCTGCTGGAGCGG 406
 35 AlAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
 407 GGGCGCTGCCCAACGACCGATAGTACGTCGGAGGCCGATCCAGGTC 456
 52 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68
 457 ATGATGATGGCAGCGCCGAGTGGCGAGGTGCTGCTGCCACGCGGC 506

68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
 507 GGAGCCCACTGGCGGACCCGACCTCTCACCCGACCCGCTGCACGACG 556
 85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
 557 CTGCGGGAGGGCTTCTTGACACGCTGTGTGTGTGTGTGTGTGTGTGT 606
 102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
 607 GCGCGGCTGACGTCGCGGATGCTGCGGCGCTGTCTGCGCGGACCTGCG 656
 118 aGluGluLeuGlyHisArgAspValAlaAArgTyrLeuArgAlaAlaAG 135
 657 TGAGGAGCTGGGCGATCGCGATGTCGACACGATACCTGCGGCGGCTCGG 706
 135 lyGlyThrArgGlySerAsnHisAlaArgTleAspAlaAlaGluGlyPro 151
 707 GGGGACACGAGGAGTAACTACCGCCGATAGTGCAGGAGGTGCC 756
 152 SerAspIleProAsp 156
 757 TCAGACATCCCGAT 771

seq_name: N_Geneseq_36.X26231

seq_documentation_block:

ID X26231 standard; DNA; 1028 BP.

AC X26231;
 DT 25-MAY-1999 (first entry)
 DE Truncated p27/p16 fusion protein encoding DNA.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 OS Homo sapiens.
 PN W0906540-A2.
 PD 11-FEB-1999.
 PF 29-JUL-1998: U15759.
 PR 29-JUL-1997: US-902572.
 PA (MITO-) MITOTIX INC.
 PI Beach DH, Gyuris J, Lamphere L;
 DR WPI: 99-153770/13.
 PT Fusion and chimaeric proteins including cyclin-dependent kinase
 binding motif - used for regulation of cell proliferation and
 differentiation, for treatment of, e.g. vascular injury, cancers,
 fibrosis and neurodegeneration
 PS Claim 60; Page 83; 88pp; English.
 CC The invention relates to novel inhibitors of cyclin-dependent kinases
 (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
 transfection system (A) that comprises: (i) first gene construct
 comprising a sequence encoding an inhibitory polypeptide containing at
 least one CDK-binding motif for binding and inhibiting activity of a CDK,
 linked to a transcription regulator functional in eukaryotic cells; (ii)
 second gene construct comprising a sequence encoding a polypeptide that
 promotes endothelialisation, and (iii) a gene delivery composition for
 delivering the Gcs to a cell for transfection. Also provided are nucleic
 acids encoding a fusion protein (FP) containing: (i) a therapeutic
 polypeptide sequence (TP) from an intracellular protein that alters a
 cellular process when FP enters the cell, and (ii) a transcellular
 polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
 consists of at least one CDK-binding motif and a TCP. See X26220 for
 detailed uses of the recombinant transfection system. The present
 sequence represents a DNA encoding a human truncated p27/p16 fusion
 protein.
 CC Sequence 1028 BP; 213 A; 308 C; 360 G; 147 T;

alignment_scores:
 Quality: 788.00 Length: 155
 Ratio: 5.117 Gaps: 0
 Percent Similarity: 99.355 Percent Identity: 99.355
 alignment_block:
 US-09-016-869A-2 x X26231
 Align seg 1/1 to: X26231 from: 1 to: 1028
 2 AspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAlaTh 18
 553 GATCCGGCGCGGGAGCAGCATGGACCTTCGCTGACTGGCTGGCCAC 602
 18 rAlaAlaAlaArgGlyArgValGluValArgAlaLeuLeuGluAlaV 35
 603 GGGCGGCGCGGGGTGCGGTAGAGGAGGTGCGGCGCTGCTGGAGGCGG 652
 35 aAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGlnVal 51
 653 GGGCGCTGCCCCAGCACCAGATAGTTACGTCGGAGCGCATCCAGGTC 702
 52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68
 703 ATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCCACGCGCG 752
 68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
 753 GGAGCCCACTGGCGGACCCGACCTCTCACCCGACCCGCTGCACGACG 802
 85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
 803 CTGCGGGAGGGCTTCTCTGACACGCTGTGTGTGTGTGTGTGTGTGTGT 852
 102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
 853 GCGGGCTGACGTCGCGGATGCTGGGGCGCTGCTGCCCTGGACCTGGC 902
 118 aGluGluLeuGlyHisArgAspValAlaAArgTyrLeuArgAlaAlaAG 135
 903 TGAGGAGCTGGGCGATCGCGATGTCGACACGATACCTGCGGCGGCTCGG 952
 135 lyGlyThrArgGlySerAsnHisAlaArgTleAspAlaAlaGluGlyPro 151
 953 GGGGACACGAGGAGTAACTACCGCCGATAGTGCAGGAGGTGCC 1002
 152 SerAspIleProAsp 156
 1003 TCAGACATCCCGAT 1017
 seq_name: N_Geneseq_36.X26232
 seq_documentation_block:
 ID X26232 standard; DNA; 1073 BP.
 AC X26232;
 DT 25-MAY-1999 (first entry)
 DE Truncated p27/p16 fusion protein encoding DNA.
 KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
 KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
 KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
 KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
 KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
 KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
 OS Homo sapiens.
 PN W0906540-A2.
 PD 11-FEB-1999.
 PF 29-JUL-1998: U15759.
 PR 29-JUL-1997: US-902572.
 PA (MITO-) MITOTIX INC.
 PI Beach DH, Gyuris J, Lamphere L;
 DR WPI: 99-153770/13.
 PT Fusion and chimaeric proteins including cyclin-dependent kinase

PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60: Page 83-84; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCS to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p21/p16 fusion
CC protein.
SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

alignment_scores:
Quality: 788.00 Length: 155
Ratio: 5.117 Gaps: 0
Percent Similarity: 99.355 Percent Identity: 99.355

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35 alAlaLeuProAsnAlaProAsnSerTyrGlyArgProIleGlnVal 51
698 GGCGCGTGCACCAACGACCAATAGTACGTCGGAGCGCGATCCAGTC 747
52 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAl 68
748 ATGATGATGGGCGGCGCGGAGTGGCGGAGCTGCTGCTCCACGGCGC 797
68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAsp 85
798 GGAGCCCACTGGCGGCGCGCGCCACTCTACCGCCGCGTGCAGCG 847
85 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGly 101
848 CTGCGCGGAGGGCTCTCTGGACGCTGGTGTGCTGCACCGCGCGG 897
102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
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118 aGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaAlaG 135
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135 IyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlyPro 151
998 GGGGACCAAGAGGACATACCATGCCCGCATAGATCCCGGAAAGTCCC 1047
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seq_name: N_Geneseq_36:T74053

seq_documentation_block:

ID T74053 standard; cDNA; 1098 BP.
AC T74053;
DT 16-MAR-1998 (first entry)
DE CDK inhibitory fusion protein p16p27 coding sequence.
KW Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 gene;
KW chimeric polypeptide; human; binding motif; proliferation control;
KW cell differentiation; cell-cycle inhibitor; proliferative disorder;
KW tissue degeneration; therapy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1098
FT /tag- a
FT WO9727297-A1.
PD 31-JUL-1997.
PF 17-JAN-1997; U00569.
PR 23-JAN-1996; US-589981.
PA (MITO-) MITOTIX INC.
PI Beach D, Gyuris J, Lamphere L;
DR WPI; 97-393685/36.
DR P-PSDB: W23536.
PT Chimeric inhibitor of cyclin dependent kinase - useful for gene
PT therapy of cancer and other proliferative and differentiative
PT diseases
PS Claim 13; Page 46-48; 58pp; English.
CC This sequence encodes a chimeric polypeptide of the invention. It was
CC derived from a fusion of the human p27 and p16 cDNA sequences. The
CC chimeric polypeptides of the invention have cyclin-dependent kinase (CDK)
CC binding motifs from at least two different proteins that bind to CDKs.
CC The protein controls proliferation and/or differentiation of cells,
CC particularly they inhibit cell-cycle progression. They can be used to
CC treat a wide range of proliferative disorders, e.g. cancer, leukaemia,
CC psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They
CC can also treat diseases associated with de-differentiation or
CC degeneration of tissue, e.g. Alzheimer's, Parkinson's or Huntington's
CC diseases, gastric ulcers and autonomous diseases of the peripheral
CC nervous system. Other applications include reducing growth of hair and
CC protecting hair follicle cells against cytotoxic treatments, cosmetically
CC to treat various forms of folliculitis, and to inhibit spermatogenesis or
CC oogenesis. The chimeric proteins can also be used in vitro to maintain
CC cells, especially neurons intended for testing specific activity of
CC trophic factors, at selected points in the cell cycle. The proteins are
CC more active inhibitors of the CDK/cyclin complex than binding motifs used
CC individually (since they may bind to CDK involved in different stages of
CC the cell cycle).
SQ Sequence 1098 BP; 234 A; 326 C; 378 G; 160 T;

alignment_scores:

Quality: 788.00 Length: 155
Ratio: 5.117 Gaps: 0
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 135 lyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyPro 151
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About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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; Patent No. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel A.
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..508
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; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: LAHIVE & COCKFIELD
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306.511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CF2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 base pairs
; TYPE: nucleic acid
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; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: FOLEY, HOAG & ELIOT LLP
; CITY: Boston
; STATE: MA
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; Patent No. 5624819

; GENERAL INFORMATION:

; APPLICANT: Skolnick, Mark H.

; APPLICANT: Cannon-Albright, Lisa A.

; APPLICANT: Kamb, Alexander

; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESSES:

; ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP

; STREET: 1201 New York Avenue, Suite 1000

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/474,177

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/03537

; FILING DATE: 17-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938

; FILING DATE: 01-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,087

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/215,086

; FILING DATE: 18-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,369

; FILING DATE: 14-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/214,582

; FILING DATE: 18-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Ihnen, Jeffrey L.

; REGISTRATION NUMBER: 28,957

; REFERENCE/DOCKET NUMBER: 24884-109348-E

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-962-4810

; TELEFAX: 202-962-8300

; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
US-08-474-177-1
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Ratio: 5.090 Gaps: 0

Percent Similarity: 99.359 Percent Identity: 98.718

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51 CACGGCGCGCGCGGGTGGGTAGAGGAGTGGCGGCGCTGCTGGAGG 100
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34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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151 GTCATGATGATGGCAGCGCGCGAGTGGCGAGTGTGCTGTCTCCACGG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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201 CGCGGAGCCCACTGCCGCCACCCGCCACTCTCACCCGACCCCGTGACG 250
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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; Sequence 1, Application US/08487033

; Patent No. 5739027

; GENERAL INFORMATION:

; APPLICANT: Kamb, Alexander

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; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,033
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
; US-08-487-033-1

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    Quality: 789.00      Length: 156
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seq_documentation_block:
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; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086

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; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
; US-08-480-810-1

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  Ratio: 5.090        Gaps: 0
  Percent Similarity: 99.359  Percent Identity: 98.718

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67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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201 CGCGAGGCCCAACTCGCGCGACCGCCGACCTCTCACCGACCGCGTGCACG 250
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301 GGGGGCGGCTGGACGTGGCGGATGCCCTGGGGCGCTGCGCCCGTGGACCT 350
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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; Sequence 1, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
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51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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84 sAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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seq_documentation_block:
Sequence 1, Application US/08848251
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GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/474,083
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA: US 08/251,938
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA: US 08/215,087
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA: US 08/215,086
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA: US 08/227,369
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA: US 08/214,582
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 1..471
US-08-848-251-1
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alignment_scores:
  Quality: 789.00      Length: 156
  Ratio: 5.090        Gaps: 0
  Percent Similarity: 99.359  Percent Identity: 98.718
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51 CACGGCGCGCGCGGGTTCGGTACGAGAGGTGCGGGCGCTGGAGG 100
|||||
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|||||
51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
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; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
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alignment_scores:
Quality: 789.00 Length: 156
Ratio: 5.090 Gaps: 0
Percent Similarity: 99.359 Percent Identity: 98.718

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51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGln 67
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151 GTCATGATGATGGCGAGCGCCGAGTGGCGAGCTGCTGCTGCCACGG 200
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis 84
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201 CGCGGAGCCCAACTGGCGAGCCCGCCACTCTCACCCGACCGTGACG 250
84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 ACCTGCCCGGGAGGCTTCTTGACACGCTGGTGTGTCACCGGGCC 300
101 GlyAlaArgLeuAspValArgAspAlaThrPglyArgLeuProValaspLe 117
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301 GGGCGCGGCTGGACGTGCGCATGCTGGGGCGCTGTCGCGGTGACCT 350
117 uAlaGluLeuGlyHisArgaspValAlaArgTyrLeuArgAlaAla 134
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; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..471
; US-09-115-252-1

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17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuGluAl 34
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51 CACGGCGCGCGCGGGGTGGGTAGAGGAGGTGGGGCGGTGGTGAGG 100

34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgProIleGln 50
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51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisG1 67
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151 GTCATGATGATGGGAGCGCGCGGAGTGGCGGAGCTGTGCTGCCACGG 200

67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
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101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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; Patent No 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERM LINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,177
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: /note= "Splice site acceptor."
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; US-08-474-177-36

alignment_scores:
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    Ratio: 5.090        Gaps: 0
    Percent Similarity: 99.359    Percent Identity: 98.718

alignment_block:
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17 aThrAlaAlaAlaArgGlyArgValGluValGluValAlaAlaLeuGluA 34
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51 CACGGCGCGCGCGGGGTCGGGTAGAGAGGTGGCGGCTGCTGGAG 100
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34 IaValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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101 CGGGGGCGCTGCCAACCGCAGCATAGTACGGTCGGAGGCCGATCCAG 150
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51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisG 67
|||||
151 GTCATGATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCTCCACGG 200
|||||
67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
|||||
201 CCGGAGGCCCACTCGCGCAGACCCGCCACTCTCACCGACCGGTGCAG 250
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84 sAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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251 AGCTGCGCGGGAGGCTCTCTGGACACGCTGGTGTGTCACCGGCC 300
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117 uAlaGluLeuLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAlaA 134
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351 GGCTGAGGAGCTGGCCATCGCGATGTCGACGATACCTGCGCGCGGCTG 400
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-36

seq_documentation_block:
; Sequence 36, Application US/08487033
; Patent No. 5735027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
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Align seg 1/1 to: US-08-487-033-36 from: 1 to: 947

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51 CACGGCCCGCGCGCGGGTTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGG 100
34 laValAlaLeuProAsnAlaProAsnSerTyrglyArgArgProIleGln 50
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VERSION	AI394605.1					
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SOURCE	human.					
ORGANISM	Homo sapiens					
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	Mammalia; Eutheria;					
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	Catarrhini; Hominoidea;					
	Homosapien					
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	Fish; Osteichthyes; Actinopterygii;					
	Clupeiformes; Clupeidae; Engraulinae;					
	Engraulis					

REFERENCE	I (bases 1 to 566)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D.

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9b_est19:AI363262	-	522.00	972.63	708	! AI363262 q25gfc11.x1 NCI CGAP_BH
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9b_est13:AA903110	-	274.00	507.83	548	! AA903110 QK52b00.s1 NCI CGAP_L

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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
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TGTTCACATCTGAATGGAGCGCGCGATGCTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
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the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldc."
113 a 159 c 175 g 118 t 1 others

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127 laArgTyrLeuArgAlaAlaAlaGlyGlyThrArgGlySerAsnHisAla 143
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316 CACGTACTTGGCGCGGCTGGCGGGGCGCAGCAGGAGCACTAACCATGCC 267
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// mRNA sequence.
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VERSION AI871381.1 GI:5545430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -40Up from Gibco
High quality sequence stop: 444.
Location/Qualifiers
1..590
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2431317"
/clone.lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTATCAATCTCAAGTGGGAGCGCGCATAGTGTGTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI

```

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 114 a 158 c 179 g 139 t
ORIGIN

alignment_scores:
Quality: 553.00 Length: 107
Ratio: 5.168 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-016-869A-2 x AI871381/rev ..

Align seg 1/1 to reverse of: AI871381 from: 1 to: 590

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50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH 66
|||||
566 CAGTCTATGATGATGGCAGCGCCAGAGTGGCGAGCTGCTGTCTCCA 517
|||||
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
516 CGGCGGAGAGCCCAACTGGCGGACCCCGCCACTCTCACCAGCCCGTGC 467
|||||
83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
|||||
466 ACAGCGCTGCCCGGAGGGTCTCTGGACACGCTGTGTGTGCACCGG 417
|||||
100 AlaGlyAlaArgLeuAspValArgAspAlaThrPlyArgLeuProValAs 116
|||||
416 GCCGGCGCGGCTGGACGTGCGGATGCCCTGGGGCGCTGTGCCCGTGA 367
|||||
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
|||||
366 CCTGCTGAGGAGCTGGCGCATCGCATGTGCGACGTTACTTGCCTGCCG 317
|||||
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
|||||
316 CTGCGGGGGGCGCAGAGGAGGAGTAACCATGCCCATAGATGCCGCGGAA 267
|||||
150 GlyProSerAspIleProAsp 156
|||||
266 GGTCCCTCAGACATCCCGCAT 246
|||||

seq_name: gb_est41:AW328496

seq_documentation_block:
LOCUS AW328496 648 bp mRNA EST 28-JAN-2000
DEFINITION ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
sequence.
ACCESSION AW328496
VERSION AW328496.1 GI:6798992
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 648)
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036295.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

```

www.bio.llnl.gov/bbrp/image/image.html
Plate: LLCW030 row: 0 column: 24
Seq primer: -21M13 forward primer (ABI).

FEATURES

source
Location/Qualifiers
1..648
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2847599"
/clone_lib="NIH_MGC_4"
/cell_line="MGC1"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Cervix; Vector: pOTB/a; Site 1: Scel;
Site 2: CeuI; cDNA made by oligo-dT priming.
Directionally cloned into CeuI/Scel sites using the
following 5' adaptor: taactaacggtcctaagtagcga and 3'
adaptor: ttctatcctctttccgcaccacataaa. Average
insert size 900 bp. Library prepared by Edge Biosystems."

BASE COUNT 127 a 200 c 196 g 123 t 2 others
ORIGIN

alignment_scores:

Quality: 553.00 Length: 107
Ratio: 5.168 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-016-869A-2 x AW328496 ..

Align seg 1/1 to: AW328496 from: 1 to: 648

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66
|||||
109 CAGGTCATGATGATGGCGAGCGCGGAGTGGCGAGCTGTGCTGCCA 158
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
159 CGGCGGAGCGCCAACTGCGCGGACCCGCCACCTCTCACCAGCCCGTGC 208
83 isAspAlaAlaArgGluGlyPheLeuLeuAspThrLeuValValLeuHisArg 99
|||||
209 ACGAGCTGCCCGGAGGCTTCCTGGACACGCTGGTGGTCTGCACCG 258
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
|||||
259 GCCGGGCGCGGCTGGACGTGCGGATGCTCTGGGCGCGCTCTGCCGTGA 308
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
|||||
309 CCTGGCTGAGGAGTGGGCCATCGGATGTCGACGCTACCTGCGCGCG 358
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
|||||
359 CTGGGGGGGCGACAGAGGAGTAACTGATGCGCCATAGATGCCCGCGAA 408
150 GlyProSerAspIleProAsp 156
|||||
409 GGTCCCTCAGACATCCCGCAT 429

seq_name: gb_est26:AI870879

seq_documentation_block:

LOCUS AI870879 579 bp mRNA EST 07-MAR-2000
DEFINITION v177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933.3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;; mRNA sequence.
ACCESSION AI870879
VERSION AI870879.1 GI:5544847
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/PTGAP), Tumor Gene Index
Unpublished (1998)
On May 18, 1998 this sequence version replaced gi:3136859.
Contact: Robert Strausberg, Ph.D.
Email: (301) 496-1550
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 819 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 474.

FEATURES

Source

Location/Qualifiers
1..579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2430933"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCATCTGAAGTGGAGCGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 157 c 182 g 127 t
ORIGIN

alignment_scores:

Quality: 541.00 Length: 107
Ratio: 5.152 Gaps: 0
Percent Similarity: 98.131 Percent Identity: 98.131

alignment_block:

US-09-016-869A-2 x AI870879/rev ..

Align seg 1/1 to reverse of: AI870879 from: 1 to: 579

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66
|||||
555 CAGGTCATGATGATGGCGAGCGCGCGGAGTGGCGAGCTGTGCTGCCA 506
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
505 CGGCGGAGCGCCAACTGCGCGGACCCGCCACCTCTCACCAGCCCGTGC 456
83 isAspAlaAlaArgGluGlyPheLeuLeuAspThrLeuValValLeuHisArg 99
|||||
455 ACGAGCTGCCCGGAGGCTTCCTGACACGCTGGTGGTGTGCACCGG 406
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
|||||
405 GCCGGGCGCGGCTGGACGTGCGGATGCTCTGGGCGCGCTCTGCCGTGA 356
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
|||||
355 CCTGGCTGAGGAGTGGGCCATCGGATGTCGACGCTACCTGCGCGCG 306

133 laAlaGlyClyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149
 |||||
 305 CTGCGGGGACCAGAGCAGTACCATGCCGATAGATGCCGGGAA 256
 |||||
 150 GlyProSerAspIleProAsp 156
 |||||
 255 GGTCCCTCAGACATCCCGAT 235

seq_name: gb_est19:AI362049

seq_documentation_block:
 LOCUS AI362049 580 bp mRNA EST 15-FEB-1999
 DEFINITION QY39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3',
 similar to TR:Q16361.Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
 ;, mRNA sequence.

ACCESSION AI362049

VERSION AI362049.1 GI:4113670

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 580)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 884 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 321.

Location/Qualifiers

FEATURES

source

1..580

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2014405"

/clone_lib="NCI_CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site1: Not I; Site2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAACTGAAGTGGAGCGCCGACATCTTTTITTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 116 a 160 c 174 g 130 t

ORIGIN

alignment_scores:

Quality: 532.00 Length: 107

Ratio: 5.067 Gaps: 0

Percent Similarity: 98.131 Percent Identity: 97.196

alignment_block:

US-09-016-869a-2 x AI362049/rev ..

Align seg 1/1 to reverse of: AI362049 from: 1 to: 580

50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 66

|||||

556 CAGGTGATGATGGGAGCGCTCGAGTGGGAGCTGCTGCTCCA 507

|||||

66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83

|||||

506 CGCGCGGAGCCCACTCGCGGACTCGCCACTCTCACCGGACCGTGC 457

|||||

83 isAspAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99

|||||

456 ACAGAGCTGCCCGGAGGCTCTCTGAACAGCTGGTGTGTCACCGG 407

|||||

100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116

|||||

406 GCCTGGCGCGGCTGGACGTGCGCGATGCTGGGCGCTGCTGCCGTGA 357

|||||

116 PleuAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133

|||||

356 CTGTGCTGAGGAGCTGGGCCATCGCGATGTGCGACGGTACCTGCGCGG 307

|||||

133 laAlaGlyClyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149

|||||

306 CTGCGGGGGGACCAGAGCGATGACCATGCCGATAGATGCCCGGAA 257

|||||

150 GlyProSerAspIleProAsp 156

|||||

256 GGTCCCTCAGACATCCCGAT 236

|||||

seq_name: gb_est17:AI198233

seq_documentation_block:

LOCUS AI198233 579 bp mRNA EST 02-DEC-1998

DEFINITION GI55612.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3',

similar to TR:Q16361.Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM

; contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI198233

VERSION AI198233.1 GI:3750839

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 579)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 729 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

Location/Qualifiers

FEATURES

source

1..579

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1860407"

/clone_lib="NCI_CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCACTCTGAAGTGGGAGCGCCGACATAGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 158 c 177 g 130 t 1 others
ORIGIN

alignment_scores:
Quality: 531.00 Length: 107
Ratio: 5.009 Gaps: 0
Percent Similarity: 99.065 Percent Identity: 96.262

alignment_block:
US-09-016-869A-2 x AI198233/rev ..

Align seg 1/1 to reverse of: AI198233 from: 1 to: 579

```
50 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66
|||||
555 CAGGTCTATGATGATGGCAGCGCCGAGTGGCGAAGCTGCTGCTGCCA 506
|||||
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
505 CAGCGCGAAGCCCAACTTCGCGGACGCGCCACTCTCACCGGACCCCTGC 456
|||||
83 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
|||||
455 ACACGCTGCGCGGAGGGCTTCCTGCACACGCTGGTGGTCTGCACCG 406
|||||
100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValas 116
|||||
405 GCGGGGCGCGGCTGGACGTCGCGGATGCTGGGGCCGCTGCGCGGGA 356
|||||
116 pLeuAlaGluGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArgAla 133
|||||
355 CTTGGCTGAGGAGCTGGGCCATCGCATGTCGCACGCTACTCGCGCGG 306
|||||
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
|||||
305 CTCGGGGGCGCACAGAGGAGTAACCATGCCCGCATAGATGCCGCGGAA 256
|||||
150 GlyProSerAspIleProAsp 156
|||||
255 GTTCCCTCAGACATCCCCGAT 235
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seq_name: gb_est25:AI765096

seq_documentation_block:
LOCUS AI765096 774 bp mRNA EST 21-DEC-1999
DEFINITION w148b08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393463 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains LTR9.b3 MER22 repetitive element ;, mRNA sequence.
ACCESSION AI765096
VERSION AI765096.1 GI:5231605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.

FEATURES
source

1..774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 153 a 220 c 221 g 179 t 1 others
ORIGIN

alignment_scores:

Quality: 529.00 Length: 158
Ratio: 4.336 Gaps: 2
Percent Similarity: 77.215 Percent Identity: 69.620

alignment_block:

US-09-016-869A-2 x AI765096/rev ..

Align seg 1/1 to reverse of: AI765096 from: 1 to: 774

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15 TrpLeuAlaThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLe 31
|||||
713 TGGTTACATCCCGGGCTCACGGGGAGG..... 684
|||||
31 uLeuGluAlaValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgp 48
|||||
683 .....TGGGCACGCCGAGGGCGGCCCGCGCTGTGGGCATCGTG 644
|||||
48 rolle..... 49
|||||
643 CTATGCTATTAGGAGCCCGAGCGTTTAGGCACGACCGCTTCCTAGAA 594
|||||
50 ...GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe 65
|||||
593 GACCAGGTCATGATGATGGCAGCGCCGCGAGTGGCGGAGCTGCTGCTGT 544
|||||
65 uHisGlyValaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 82
|||||
543 CCACGGCGCGGAGCCCAATTGGCGCGACCCGCCCACTTCCACCCGACCG 494
|||||
82 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 98
|||||
493 TGCACGACGCTGCCCGGAGGGCTTCCTGCACAGCTGGTGGTCTGCAC 444
|||||
99 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 115
|||||
443 CGGGCCCGGGCGGCTGGACGTCGCGCAATCCCTGGGGCGGCTGCCCCGT 394
|||||
115 lAspLeuAlaGluLeuGlyHisArgAspValAlaAlaArgTyrLeuArg 132
|||||
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```

393 GGACCTGGCTGAGGAGCTGGGCCATCGCATGTCGCCCGGTACCTGCGCG 344
132 laalaalaGlyThrArgGlySerAsnHisAlaArgIleAspAlaA 148
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
343 CGGCTCGGGGGGCCACGAGCGAGTAAACATGCCCGCATAAATGCCGCG 294
149 GluGlyProSerAspIleProasp 156
293 GAAGTCCCTCAGACATCCCCGAT 270
seq_name: gb_est25:AI817709

seq_documentation_block:
LOCUS AI817709 729 bp mRNA 21-DEC-1999
DEFINITION WK25C11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA
sequence.
ACCESSION AI817709
VERSION AI817709.1 GI:5436788
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
REFERENCE
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3035534.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Insert Length: 848 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 468.
FEATURES
Location/Qualifiers
1..729
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2413364"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATAGTGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 141 a 214 c 226 g 143 t 5 others
ORIGIN

alignment_scores:
Quality: 526.00 Length: 171
Ratio: 4.015 Gaps: 4
Percent Similarity: 76.608 Percent Identity: 67.251

alignment_block:
US-09-016-869A-2 x AI817709/rev ..
Align seg 1/1 to reverse of: AI817709 from: 1 to: 729
2 AspProAlaAlaGlySerMetGluProSerAlaAspTTrpLeuAlaTh 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 GACCTCCGNATTCGGCGCGGTCCGNCCTCCTAGAACACAGGTCATG 546
18 talaalaalaArgGlyArgValGluGluValArgAlaLeuLeuGluAla 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
694 .GCCGCGAGTGAGGGTTCGTGGTTTCATCCGCGNGCTCACGGGGAGT 646
35 ValAlaLeuProAsnAlaPro..... 41
||| |||:|||||
645 GGGCGACGCGCCAGGCGCGCCGCGCTGTCGCTGCTGCTGCTACT 596
42 .....AsnSerTyrGlyArgProIleGlnValMetMet..... 53
||| |||:|||||
595 GAGACCCCGAGCTGAGGCGACGCCCTTCCTAGAACACAGGTCATG 546
54 ..MetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaGlu 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
545 ATGATGGCAGCGCCGAGTGGCGGAGTGTCTGCTCCACGGCGCGGAG 496
70 ProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAla 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
495 CCCAACTCGCGGACNCCGCCACTCTCACCGACCCGCTGCACGCGCTGC 446
86 aArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
445 CGGGAGGCGTCTCTGGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
103 tGLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGlu 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
395 GGTGGACGTGCGGATGCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTG 346
120 GluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaAlaGlyG 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
345 GAGCTGGGCCATCGGATGTCGACGGTACCTGCGCGCGCTGCGGGGG 296
136 YThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyProSer 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
295 CACACAGAGCAGTACCATGCCCCGATAGATGCCGCGGAGGTCCTCTC 246
153 spIleProasp 156
|||||:|||||
245 ACATCCCGCAT 235
seq_name: gb_est19:AI363262
seq_documentation_block:
LOCUS AI363262 708 bp mRNA EST 16-FEB-1999
DEFINITION qy56f03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3'
similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ;contains
LTR9_b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI363262
VERSION AI363262.1 GI:4114883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
REFERENCE
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

```

cdNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cdNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
Insert length: 872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.

FEATURES

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1. .708
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TTTACCAATCGAAGTGGCGCCGATATCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 137 a 210 c 219 g 140 t 2 others
ORIGIN

alignment_scores:
Quality: 522.00 Length: 107
Ratio: 5.019 Gaps: 0
Percent Similarity: 97.196 Percent Identity: 95.327

alignment_block:

US-09-016-869A-2 x AI363262/rev ..
Align seg 1/1 to reverse of: AI363262 from: 1 to: 708
50 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuH1 66
|||||
540 CAGGTCATGATGATGGCAAGCGCCGAGTGGCGAGCTGCTGCTCCC 491
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
|||||
490 GGGCGGGAGCCCAACTCGGACGACCCGCCCACTCTCACCAGCCCGTGC 441
83 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
|||||
440 ACGACGCTGCCCGGAGGGCTCTCTGGACACGCTGCTGCTGCACCGG 391
100 AlaGlyAlaArgLeuAspValArgAspAlaArgGlyArgLeuProValAs 116
|||||
390 GCCGGGGCGGCTGACGTGGCGCATGCTGGGGCCGCTCTGCCCGCTGA 341
116 pLeuAlaGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
|||||
340 CCTGGCTGAGGAGCTGGCCCATCGGATGTCGACGGTACCTGCGCGGG 291
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149
|||||
290 CTGCGGGGGACCAAGAGCGCATACCATGCCCCGATAGATGTCGCCGAA 241
150 GlyProSerAspIleProAsp 156
|||||
240 GGTCCCTCAGACATCCCGAT 220

seq_name: gb_est27:AI954684

seq_documentation_block:

LOCUS AI954684 563 bp mRNA EST 08-MAR-2000

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

wq34hl2 x1 NCI-CGAP GC6 Homo sapiens cdNA clone IMAGE:2473223 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A ; mRNA sequence.

AI954684

AI954684.1 GI:5746994

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cdNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert length: 613 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 460.

Location/Qualifiers

1. .563

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2473223"

/clone_lib="NCI-CGAP GC6"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Plasmid DNA from the normalized library

NCI-CGAP GC4 was prepared, and as circles were made in

vitro. Following HAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from a pool of 5,000 clones made

from the same library (cloneIDs 1257096-1258631,

1469064-1470983, and 1475592-1476743). Subtraction by

Bento Soares and M. Fatima Bonaldo."

BASE COUNT 112 a 158 c 169 g 124 t

ORIGIN

alignment_scores:

Quality: 514.00 Length: 111

Ratio: 4.849 Gaps: 0

Percent Similarity: 95.495 Percent Identity: 94.595

alignment_block:

US-09-016-869A-2 x AI954684/rev ..

Align seg 1/1 to reverse of: AI954684 from: 1 to: 563

46 ArgArgProIleGlnValMetMetGlySerAlaArgValAlaGluLe 62

|||||

563 AGGCCAAATGTAGGGGTCATGATGGGCGAGCCCGAGTGGCGGAGCT 514

62 uLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeu 79

|||||

513 CTGCTGCTCCACGGCGGAGCCCACTG.GCCGACCCGCCCACTCTCA 465

79 hrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLeuVal 95

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464 CCCGACCGCTGCACGACGCTGCCGGGAGGGCTTCTCTGGACACGCTGGTG 415


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/tissue.type="pooled germ cell tumors"
/lab_host="DH10B"
/notes=vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clonids 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaudo.
BASE COUNT 107 a 144 c 163 g 116 t 1 others
ORIGIN

alignment_scores:
  Quality: 506.00 Length: 99
  Ratio: 5.163 Gaps: 0
  Percent Similarity: 98.990 Percent Identity: 98.990

alignment_block:
US-09-016-869A-2 x AI633790/rev ..
Align seg 1/1 to reverse of: AI633790 from: 1 to: 531

58 ArgValAlaGluLeuLeuHisGlyAlaGluProAsnCysAlaAs 74
531 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGCGA 482
74 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 91
481 CNCCGCCACTCTCACCGACCCGTGCAGACGCTGCCGGGAGGGCTTCC 432
91 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 107
431 TGGACACGCTGGTGTGTCACCGCGCGCGCGCTGCAGCTGCGC 382
108 AspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisAr 124
381 GATGCCCTGGGGCCGCTGCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 332
124 gAspValAlaArgTyrLeuArgAlaAlaGlyGlyThrArgGlySerA 141
331 CGATGTGCACGATACCTGCGCGCGGCTGCGGGGGACACAGAGGCAGTA 282
141 snHisAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
281 ACCATGCCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGCAT 235

seq_name: gb_est23:AI638416

seq_documentation_block:
LOCUS AI638416 528 bp mRNA 14-DEC-1999
DEFINITION tt31q03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaudo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 648 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.

FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2242420"
/clone_lib="NCI_CGAP_GC6"
/tissue.type="pooled germ cell tumors"
/lab_host="DH10B"
/notes=vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (clonids 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaudo.
BASE COUNT 106 a 143 c 163 g 114 t 2 others
ORIGIN

alignment_scores:
  Quality: 502.00 Length: 99
  Ratio: 5.122 Gaps: 0
  Percent Similarity: 98.990 Percent Identity: 97.980

alignment_block:
US-09-016-869A-2 x AI638416/rev ..
Align seg 1/1 to reverse of: AI638416 from: 1 to: 528

58 ArgValAlaGluLeuLeuHisGlyAlaGluProAsnCysAlaAs 74
528 CGAGTGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGNGA 479
74 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 91
478 CNCCGCCACTCTCACCGACCCGTGCAGACGCTGCCGGGAGGGCTTCC 429
91 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 107
428 TGGACACGCTGGTGTGTCACCGCGCGCGGCGCTGCAGCTGCGC 379
108 AspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuGlyHisAr 124
378 GATGCCCTGGGGCCGCTGCTGCCGTGGACCTGCAGGAGCTGGGCCATCG 329
124 gAspValAlaArgTyrLeuArgAlaAlaGlyGlyThrArgGlySerA 141
328 CGATGTGCACGATACCTGCGCGCGGCTGCGGGGGACACAGAGGCAGTA 279
141 snHisAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
278 ACCATGCCGCATAGATGCCCGGAAGGTCCCTCAGACATCCCGCAT 232

seq_name: gb_est36:AW006218

seq_documentation_block:
LOCUS AW006218 579 bp mRNA 10-SEP-1999
DEFINITION wz93q05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566424 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
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ACCESSION      AW006218
VERSION        AW006218.1  GI:5854996
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 579)
AUTHORS        NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute / National Institute of Neurological
               Disorders and Stroke, Brain Tumor Genome Anatomy Project
               (CGAP/BTGP), Tumor Gene Index
JOURNAL        Unpublished (1998)
COMMENT        On Oct 6, 1998 this sequence version replaced gi:3705694.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert_Strausberg@nih.gov
               Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
               Ph.D. Library Preparation: M. Bento Soares, Ph.D., M. Fatima
               Bonaldo, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Seq primer: -40UP from Gibco
               High quality sequence stop: 461.
FEATURES       Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone_lib="NCI-CGAP_Brn25"
               /lab_host="DH10B"
               /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
               modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
               strand cDNA was primed with a Not I - oligo(dT) primer [5'
               TGTTACCAATCTGAAGTGGAGCGCGCATAGTTTGTGTTTTTTTTTTTTTTT
               T 3']; double-stranded cDNA was ligated to Eco RI
               adaptors (Pharmacia), digested with Not I and cloned into
               the Not I and Eco RI sites of the modified pT73 vector.
               Library is normalized, and was constructed by Bento
               Soares and M. Fatima Bonaldo."
BASE COUNT     113 a 161 c 172 g 131 t
ORIGIN
alignment_scores
  Quality: 484.00      Length: 107
  Ratio: 4.654         Gaps: 0
  Percent Similarity: 97.196 Percent Identity: 95.327
alignment_block:
us-09-016-869a-2 x AW006218/rev ..
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554 AAGGTGATGATGATGAGGAGCGCCGAGG.GCGGAGCTGCTGCTGCTCA 506
   ::::::::::::::::::::::::::::::::::::::::::::::
66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
   ::::::::::::::::::::::::::::::::::::::::::::::
505 CGGGNGGAGCCCAANTGCGGACCGCC.ACTCTCACCCGACCGGTGC 457
   ::::::::::::::::::::::::::::::::::::::::::::::
83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
   ::::::::::::::::::::::::::::::::::::::::::::::
456 ACGACGCTCCCGGAGGGCTTCTGACACGCTGCTGCTGTCACCGG 407
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100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
   ::::::::::::::::::::::::::::::::::::::::::::::
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406 CCCGGGGCGGCTGGACGTGGCGGATCCCTGGGGCCCTGTCGCCGTGGA 357
116 pleuAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAla 133
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356 CTTGCTGAGGAGCTGGGCCATCGGATGTCGACGGTACCTGGCGCGG 307
133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaGlu 149
   ::::::::::::::::::::::::::::::::::::::::::::::
306 CTGCGGGGGGACCAGAGCAGTACCATGCCGCGCATAGATGCCGCGGAA 257
150 GlyProSerAspIleProAsp 156
   ::::::::::::::::::::::::::::::::::::::
256 GGTCCCTCAGACATCCCGAT 236
seq_name: gb_est9:AA557137
seq_documentation_block:
LOCUS      AA557137      599 bp      mRNA      EST      09-SEP-1997
DEFINITION n174505.s1 NCI-CGAP_Br2 Homo sapiens cDNA clone IMAGE:1056369 3',
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; mRNA sequence.
ACCESSION  AA557137
VERSION    AA557137.1  GI:2327614
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 599)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    On Jan 14, 1998 this sequence version replaced gi:1877968.
               Contact: Robert Strausberg, Ph.D.
               Tel: (301) 496-1550
               Email: Robert_Strausberg@nih.gov
               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
               Emmert-Buck, M.D., Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Insert Length: 755 Std Error: 0.00
               Seq primer: -40ml3 fwd. Et from Amersham
               High quality sequence stop: 410.
FEATURES    Location/Qualifiers
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="NCI-CGAP_Br2"
               /sex="female, pooled"
               /tissue_type="breast"
               /lab_host="DH10B"
               /note="Vector: pT73D-Pac (Pharmacia) with a modified
               polylinker; 1st strand cDNA was prepared from pooled bulk
               breast tumor tissue, and was then primed with a Not I -
               oligo(dT) primer. Double-stranded cDNA was ligated to Eco
               RI adaptors (Pharmacia), digested with Not I and cloned
               into the Not I and Eco RI sites of the modified pT73
               vector. This library is the normalized version of
               NCI CGAP_Brl.1. Library was constructed by Bento Soares
               and M. Fatima Bonaldo."
BASE COUNT  123 a 163 c 179 g 134 t
ORIGIN
alignment_scores
  Quality: 484.00      Length: 119
  Ratio: 4.209         Gaps: 1
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Percent Similarity: 96.639   Percent Identity: 88.235
alignment_block:
US-09-016-869A-2 x AA557137/rev  ..

Align seg 1/1 to reverse of: AA557137 from: 1 to: 599

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587 CAGCACCGAATAGTTACGGTCGGAGCCGATTCAAGTTCAGATTGATGG 538

55  ySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnC 72
   |::: |:::::::::::::::::::::::: |:::::::::::::
537 CCAGCCCCGAATGCGGAATGCTGCTGCTCCAGGC.GCGAGGCCCAAT 489

72  ysAlaAspProAlaThrLeuThrArgProValHisAspAlaAlaArgGlu 88
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488 GCGCCGACCCCGCAATCTCACCCGACCCGTCGACGAGACGCTGCCCGGAG 439

89  GlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAs 105
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438 GGCTTCTTGACACGCTGGTGGTGGTGCACCGCGCGCGGGCGGCTGGA 389

105 pValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGluLeuG 122
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388 CGTGC CGCATGCCCTGGGC.CGTCTGCCCTGGACCTGGCTGAGGAGCTGG 340

122 lyHisArgAspValAlaArgTyr.LeuArgAlaAlaAlaGlyGlyThr 138
   |::| | | | | | | | | | | | | | | | | | | | | | | |
339 GCCATTGCGATGTCGCACGGTACTCTCGCGCGGCTCGCGGGGGCACAG 290

138 gGlySerAsnHisAlaArgIleAspAlaAlaGluGlyProSerAspIle 155
   | | | | | | | | | | | | | | | | | | | | | | | |
289 AGCAGTPAACCATGCCCGCATAGATCCCGGGAAGGTCCCTCAGACATCC 240

155 roAsp 156
   | | | |
239 CCGAT 235

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:04:57 ; Search time 2513.97 Seconds
(without alignments)
594.196 Million cell updates/sec

Title: US-09-016-869A-3

Perfect score: 837

Sequence: 1 GAGGACTCCGCGACGGTCCG.....AGGCTGCCAACGGGAGCGG 837

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba1.*
2: gb_ba2.*
3: gb_om.*
4: gb_ov.*
5: gb_pat.*
6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pl3.*
10: gb_pr2.*
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19: em_in.*
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21: em_or.*
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24: em_ph.*
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26: em_ro.*
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28: em_sy.*
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38: em_hum4.*
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44: gb_htg7.*
45: em_htg1.*
46: em_htg2.*
47: em_htg3.*
48: em_hum5.*
49: gb_pl3.*
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51: gb_htg8.*
52: gb_htg9.*
53: gb_htg10.*
54: gb_htg11.*
55: gb_htg12.*
56: gb_htg13.*
57: gb_htg14.*
58: gb_in3.*
59: gb_htg15.*
60: gb_htg16.*
61: gb_htg17.*
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63: em_htg5.*
64: em_htg6.*
65: em_htg7.*
66: em_hum6.*
67: gb_htg18.*
68: gb_htg19.*
69: gb_htg20.*
70: gb_htg21.*
71: gb_htg22.*
72: gb_htg23.*
73: gb_htg24.*
74: gb_htg25.*
75: gb_htg26.*
76: gb_htg27.*
77: gb_htg28.*
78: gb_htg29.*
79: gb_htg30.*
80: gb_htg31.*
81: gb_v11.*
82: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	837	100.0	837	9	HUMCIP	L36844 Homo sapien
2	677.2	80.9	751	5	AR001326	AR001326 Sequence
3	677.2	80.9	751	5	AR037506	AR037506 Sequence
4	677.2	80.9	751	5	AR062786	AR062786 Sequence
5	677.2	80.9	751	5	I41160	I41160 Sequence 15
6	672	80.3	738	11	HSU17075	U17075 Human p14-C
7	540.2	64.5	859	11	AF004819	AF004819 Homo sapi
8	418.2	50.0	753	39	S75756	S75756 p13-cyclin
9	418.2	50.0	44160	39	AC000049	AC000049 Homo sapi
10	360	43.0	457	39	S69805	S69805 MTS2-multip
11	360	43.0	1244	5	AR001317	AR001317 Sequence
12	360	43.0	1244	5	AR037497	AR037497 Sequence
13	360	43.0	1244	5	AR062777	AR062777 Sequence
14	360	43.0	1244	5	I41151	I41151 Sequence 5
15	330.4	39.5	2147	39	AF058758	AF058758 Homo sapi
16	278.4	33.3	1301	12	AF059567	AF059567 Mus muscu
17	277	33.1	706	12	S79760	S79760 Ink4 I rats,
18	266.8	31.9	471	5	AR001314	AR001314 Sequence
19	266.8	31.9	471	5	AR037494	AR037494 Sequence
20	266.8	31.9	471	5	AR062774	AR062774 Sequence
21	266.8	31.9	471	5	I41148	I41148 Sequence 1
22	266.8	31.9	947	5	AR001346	AR001346 Sequence
23	266.8	31.9	947	5	AR037526	AR037526 Sequence
24	266.8	31.9	947	5	AR062806	AR062806 Sequence

25 266.8 31.9 947 5 I41180
26 266.8 31.9 987 10 HUMINK4X
27 265.6 31.7 1420 5 I67718
28 265.4 31.7 393 5 AR062815
29 251.4 30.0 742 20 AB010808
30 232 27.7 660 11 S78535
31 232 27.7 1017 10 HSU26727
32 232 27.7 1131 5 AR001325
33 232 27.7 1131 5 AR037505
34 232 27.7 1131 5 AR062785
35 232 27.7 1131 5 I41159
36 230.6 27.6 457 39 S69804
37 230.6 27.6 540 39 S69822S1
38 230.6 27.6 585 11 HSPCDK2
39 230.6 27.6 1187 5 AR001316
40 230.6 27.6 1187 5 AR037496
41 230.6 27.6 1187 5 AR062776
42 230.6 27.6 1187 5 I41150
43 230.6 27.6 34669 39 AC000048
44 230.4 27.5 905 10 HSU38945
45 229.8 27.5 793 39 AF115544

ALIGNMENTS

RESULT 1
HUMCIP HUMCIP 837 bp mRNA PRI 08-OCT-1994
LOCUS Homo sapiens (clone p15INK4B/HA5) CDK inhibitory protein mRNA,
DEFINITION complete cds.
ACCESSION L36844
VERSION L36844.1 GI:556197
KEYWORDS CDK inhibitory protein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 837)
AUTHORS Hannon,G.J. and Beach,D.
TITLE p15INK4B is a potential effector of TGF-beta induced cell cycle
arrest
JOURNAL Nature 371, 257-261 (1994)
MEDLINE 94359613
FEATURES Location/Qualifiers
source 1..837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HsCat"
/cell_type="keratinocyte"
/clone="p15INK4B/HA5"
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328..741
/codon_start=1
/product="CDK inhibitory protein"
/protein_id="AAA50282.1"
/db_xref="GI:556198"
/translation="MREKNKMPGSGGSGDEGLATPARGLVKRVHSWEAGADPNVNR
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742..837
3'UTR 152 a 258 c 304 g 123 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.2e-129;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GAGGACTCCGCGACGTCGCGACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCCG 60

QY 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCCCGCTGTGTTCTTTGAGCGCCAGGA 120
DB 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGCGCGCCCGCTGTGTTCTTTGAGCGCCAGGA 120
QY 121 AAAGCCCGGAGCTACGACCGCGCGCTCGGCACTGCACGGGCGCCCAAGCGCGCAAGAA 180
DB 121 AAAGCCCGGAGCTACGACCGCGCGCTCGGCACTGCACGGGCGCCCAAGCGCGCAAGAA 180
QY 181 GGACGACCGGAGGTAATGAAGCTGAGCCAGTCTCTCTAGGAAGGAGAGTAGTGGCGCGG 240
DB 181 GGACGACCGGAGGTAATGAAGCTGAGCCAGTCTCTCTAGGAAGGAGAGTAGTGGCGCGG 240
QY 241 AGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCCAACGCTGATATATCCG 300
DB 241 AGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCCAACGCTGATATATCCG 300
QY 301 GCGCGCTCGGCTGTGGGGCTGCGGAATGCGGAGGAGAGACAGGGCATGCCAGTGGG 360
DB 301 GCGCGCTCGGCTGTGGGGCTGCGGAATGCGGAGGAGAGACAGGGCATGCCAGTGGG 360
QY 361 GCGCGCAGCATGAGGGTCTGGCCACGCGCGCGGGGACTAGTGGAAGGTGCGACAC 420
DB 361 GCGCGCAGCATGAGGGTCTGGCCACGCGCGCGGGGACTAGTGGAAGGTGCGACAC 420
QY 421 TCCTGGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGCGATCCAG 480
DB 421 TCCTGGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGCGCGCGATCCAG 480
QY 481 GTCATGATGAGGCGCGCGCGCGCTGCGGAGTCTGCTGCTCCAGCGCGCGAGGCC 540
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QY 601 CTGGACACGCTGGTGTGCTGCACCGCGCGCGCGCGCGGTGGAGCTGCGCGATGCTCTGG 660
DB 601 CTGGACACGCTGGTGTGCTGCACCGCGCGCGCGCGCGGTGGAGCTGCGCGATGCTCTGG 660
QY 661 GGTGCTGCGCGCTGGACTTGGCGGAGGAGCGCGCGCGCGCGCGGTGGAGCTGCGAGGTACCTG 720
DB 661 GGTGCTGCGCGCTGGACTTGGCGGAGGAGCGCGCGCGCGCGCGGTGGAGGTACCTG 720
QY 721 GCGCAGCAGCGGCGGACTGACCGCAGGTTCGCCAGCGCGCGCGCGCGCGGTTCCTTTCT 780
DB 721 GCGCAGCAGCGGCGGACTGACCGCAGGTTCGCCAGCGCGCGCGCGCGGTTCCTTTCT 780
QY 781 TACCAATTTCCACCCCG 837
DB 781 TACCAATTTCCACCCCG 837

RESULT 2

AR001326 751 bp DNA PAT 04-DEC-1998
LOCUS Sequence 15 from patent US 5739027.
DEFINITION AR001326
ACCESSION AR001326
VERSION AR001326.1 GI:3963393
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 751)
AUTHORS Kamb,A.
TITLE MSL1L.beta. gene
JOURNAL Patent: US 5739027-A 15 14-APR-1998;
FEATURES Location/Qualifiers
source 1..751
BASE COUNT 130 a 225 c 292 g 104 t
ORIGIN

FEATURES		Location/Qualifiers	
source		1..751	
BASE COUNT		130 a 225 c 292 g 104 t	
ORIGIN			
Query Match 80.9%; Score 677.2; DB 5; Length 751;			
Best Local Similarity 97.9%; Pred. No. 7.6e-103;			
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;			
QY	1	GAGGACTCCGCGACG-GTCCGACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
Db	9	GAGGACTCCGCGACGCGTCCGACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCGTCC	68
QY	60	GCCTAGGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
Db	69	GCCTAGGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACGACCGCCGCTCGG-CACGTGACGGGGCCCCAAGCCGAGAG	178
Db	129	AAAGCCCGGAGCTAACGACCGCCGCTCGGCACTGCAAGGGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGGAGGCTAATGAGCTGAGCCAGGTCTCTTAGGAAGGAGAGAGTGCGCC	238
Db	186	AAGGACGCGGGAGGCTAATGAGCTGAGCCAGGTCTCTTAGGAAGGAGAGAGTGCGCC	245
QY	239	GGAGCAGCGTGGGAAAGAGGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
Db	246	GGAGCAGCGTGGGAAAGAGGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	305
QY	299	CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
Db	306	CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGGCGGACGATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
Db	366	GGGGCGGACGATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
Db	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCCAGGTCTATGATGATGGGAGCGCGCGGCTGCGGAGTGTCTGCTTCCACGGCGGG	535
Db	486	TCCAGGTCTATGATGATGGGAGCGCGCGGCTGCGGAGTGTCTGCTTCCACGGCGGG	545
QY	536	AGCCCAACTGCGCAGACCTTCCACCTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
Db	546	AGCCCAACTGCGCAGACCTTCCACCTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGGCTGGAGCTGCGCGATG	655
Db	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTGTGCCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGAGCTTGCAGGGT	715
Db	666	CCTGGGGTCTGTGCCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGAGCTTGCAGGGT	725
QY	716	ACCTGGCAGACGACCGGGGACTGA 741	
Db	726	ACCTGGCAGACGACCGGGGACTGA 751	
RESULT 4			
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LOCUS	AR062786	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5843756.		
ACCESSION	AR062786		
VERSION	AR062786.1 GI:5990477		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	ORGANISM		
29-SEP-1999			

Query Match 80.9%; Score 677.2; DB 5; Length 751;		DB 5; Length 751;	
Best Local Similarity 97.9%; Pred. No. 7.6e-103;		Pred. No. 7.6e-103;	
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;		Mismatches 8; Indels 8; Gaps 4;	
QY	1	GAGGACTCCGCGACG-GTCCGACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC	59
Db	9	GAGGACTCCGCGACGCGTCCGACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCGTCC	68
QY	60	GCCTAGGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	119
Db	69	GCCTAGGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG	128
QY	120	AAAGCCCGGAGCTAACGACCGCCGCTCGG-CACGTGACGGGGCCCCAAGCCGAGAG	178
Db	129	AAAGCCCGGAGCTAACGACCGCCGCTCGGCACTGCAAGGGGCCCAAGCCGC---AG	185
QY	179	AAGGACGCGGGAGGCTAATGAGCTGAGCCAGGTCTCTTAGGAAGGAGAGAGTGCGCC	238
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QY	239	GGAGCAGCGTGGGAAAGAGGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATC	298
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QY	299	CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTG	358
Db	306	CGGGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTG	365
QY	359	GGGGCGGACGATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	415
Db	366	GGGGCGGACGATGAGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAAGGTGC	425
QY	416	GACACTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	475
Db	426	GACAGCTCTCTGGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGA	485
QY	476	TCCAGGTCTATGATGATGGGAGCGCGCGGCTGCGGAGTGTCTGCTTCCACGGCGGG	535
Db	486	TCCAGGTCTATGATGATGGGAGCGCGCGGCTGCGGAGTGTCTGCTTCCACGGCGGG	545
QY	536	AGCCCAACTGCGCAGACCTTCCACCTCTCACCGCGCGGCTGGAGCTGCGCGATG	595
Db	546	AGCCCAACTGCGCAGACCTTCCACCTCTCACCGCGCGGCTGGAGCTGCGCGATG	605
QY	596	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGGCTGGAGCTGCGCGATG	655
Db	606	GCTTCTTGACACGCTGGTGTCTGCACCGCGCGCGGCTGGAGCTGCGCGATG	665
QY	656	CCTGGGGTCTGTGCCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGAGCTTGCAGGGT	715
Db	666	CCTGGGGTCTGTGCCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGAGCTTGCAGGGT	725
QY	716	ACCTGGCAGACGACCGGGGACTGA 741	
Db	726	ACCTGGCAGACGACCGGGGACTGA 751	
RESULT 3			
AR037506			
LOCUS	AR037506	751 bp	DNA
DEFINITION	Sequence 15 from patent US 5801236.		
ACCESSION	AR037506		
VERSION	AR037506.1 GI:5955362		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 751)		
AUTHORS	Kamb, A.		
TITLE	Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes		
JOURNAL	Patent: US 5801236-A 15 01-SEP-1998;		


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RESULT 6
HSU17075      738 bp  mRNA      PRI
DEFINITION   Human p14-CDK inhibitor mRNA, complete cds.
ACCESSION   U17075
VERSION     U17075.1 GI:639715
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 738)
AUTHORS    Guan,K.L., Jenkins,C.W., Li,Y., Nichols,M.A., Wu,X., O'Keefe,C.L.,
            Matera,A.G. and Xiong,Y.
TITLE      Growth suppression by p18, a p16INK4/MTS1- and
            p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type prb
            function.
JOURNAL    Genes Dev. 8 (24), 2939-2952 (1994)
MEDLINE    95095079
AUTHORS    Guan,K.
DIRECT SUBMISSION
            Submitted (09-NOV-1994) Kun-Liang Guan, Biological Chemistry,
            University of Michigan, 1301 East Catherine, Ann Arbor, MI 48109,
            USA
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BASE COUNT   127 a 223 c 286 g 102 t
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Query Match      80.3%; Score 672; DB 11; Length 738;
Best Local Similarity 97.8%; Pred. No. 5.5e-102;
Matches 714; Conservative 0; Mismatches 10; Indels 6; Gaps 3;
QY 16 GTCCGCACCTCGCGCCAGAGCGCTTTGAGCTCGGCTGCTCCGCGCTAGCGCTTTT 75
Db 11 GTCCGCACCTCGCGCCAGAGCGCTTTGAGCTCGGCTGCTCCGCGCTAGCGCTTTT 70
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Db 71 CCAGAAAGCAATCCAGCGCGCGCTGCTTCTTGAGCCCGAGAAACCCCGAGCTAA 130
QY 136 CGACCGCGCGCTCGG--CACTGCACGGGGCCCAAGCCCGAGAGAGAGAGCGAGGG 194
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QY 195 TAATGAAGCTGAGCCAGCTCTCTAGGAAGGAGAGAGTGCGCCGAGCAGCGTGGGAA 254
Db 189 TAATGAAGCTGAGCCAGCTCTCTAGGAAGGAGAGAGTGCGCCGAGCAGCGTGGGAA 248
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Db 249 GAAGGAAGAGTCTCTTAAGTTTACGGCAACCGGTGGATTATCCGGGCGCTGCGCGTC 308
QY 315 TGGGGGCTCGGAATCGCGAGAGAGAACAGAGCGCATGCCAGTGGGGCGGACGCGATGA 374
Db 309 TGGGGGCTCGGAATCGCGAGGAGAGAACAGAGCGCATGCCAGTGGGGCGGACGCGATGA 368
QY 375 GGGTCTGGGCA---CCCGCGCGGGGACTAGTGGAGAGGTCGGACACTCTCTGGGAAGC 431
Db 369 GGGTCTGGCAGCGCGCGGGGACTAGTGGAGAGAGGTCGGACACTCTCTGGGAAGC 428
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QY 432 CGGCGCGGATCCAAAGGAGTCAACCGTTTCGGAGGCGCGCATCCAGTGATGATGAT 491
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QY 492 GGGCAGCGCGCGCGTGGGGAGCTGCTGCTGCACGGCGGGAGCCCAACTGGCAGA 551
Db 489 GGGCAGCGCGCGCGTGGGGAGCTGCTGCTGCACGGCGGGAGCCCAACTGGCAGA 548
QY 552 CCCTGCACCTCTCACCCGACCGGTGCATGCTGCCGGGAGGGCTTCTTGACACAGCT 611
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QY 732 GGGGGACTGA 741
Db 729 GGGGGACTGA 738
RESULT 7
AF004819      859 bp  mRNA      PRI
DEFINITION   Homo sapiens alternative spliced form of p15 CDK inhibitor mRNA,
            complete cds.
ACCESSION   AF004819
VERSION     AF004819.1 GI:2257934
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 859)
AUTHORS    Tsubari,M., Tihoonen,E. and Laiho,M.
TITLE      Cloning and characterization of p10, an alternatively spliced form
            of p15 cyclin-dependent kinase inhibitor
            Cancer Res. 57 (14), 2966-2973 (1997)
JOURNAL    97373727
MEDLINE
REFERENCE   2 (bases 1 to 859)
AUTHORS    Tsubari,M., Tihoonen,E. and Laiho,M.
TITLE      Direct Submission
            Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
            University of Helsinki, P.O. Box 21, Helsinki 00014, Finland.
JOURNAL
FEATURES
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Best Local Similarity 83.8%; Pred. No. 2.9e-80;
Matches 715; Conservative 0; Mismatches 8; Indels 130; Gaps 4;
QY 16 GTCCGCACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCCGCGCTAGCGCTTTT 75
Db 10 GTCCGCACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCCGCGCTAGCGCTTTT 69
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QY 658 TGGGTCGCTGCTGCCGTGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTGCAGGGTAC 717
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Db 451 TGGGGTCGCTGCCGTGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTGCAGGGTAC 510
|||||
QY 718 CTGCGCACAGCCACGGGGAGCTGACGCCAGGTTCCCGACGCGCCCAACAGCACTTTATT 777
|||||
Db 511 CTGCGCACAGCCACGGGGAGCTGACGCCAGGTTCCCGACGCGCCCAACAGCACTTTATT 570
|||||
QY 778 TCTTACCCCAATTTCCACACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837
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Db 571 TCTTACCCCAATTTCCACACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630
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RESULT 14
I41151
LOCUS I41151 1244 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 5 from patent US 5624819.
ACCESSION I41151
VERSION I41151.1 GI:2081741
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germ-line mutations in the MTS gene
JOURNAL Patent: US 5624819-A 5 29-APR-1997;
FEATURES Location/Qualifiers
source 1..1244
BASE COUNT 279 a 343 c 355 g 260 t 7 others
ORIGIN
Query Match 43.0%; Score 360; DB 5; Length 1244;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTATGATGATGGCAGCGCCCGCTGGCGAGCTGCTGCTCCACGCGCGGAG 537
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QY 658 TGGGTCGCTGCCGTGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTGCAGGGTAC 717
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Db 451 TGGGTCGCTGCCGTGACTTGGCCGAGGAGCGGGGCCACCGGACGCTTGCAGGGTAC 510
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QY 718 CTGCGCACAGCCACGGGGAGCTGACGCCAGGTTCCCGACGCGCCCAACAGCACTTTATT 777
|||||
Db 511 CTGCGCACAGCCACGGGGAGCTGACGCCAGGTTCCCGACGCGCCCAACAGCACTTTATT 570
|||||
QY 778 TCTTACCCCAATTTCCACACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837
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Db 571 TCTTACCCCAATTTCCACACCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630
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RESULT 15
AF058758
LOCUS AF058758 2147 bp DNA PRI 29-JAN-2000
DEFINITION Homo sapiens cyclin-dependent kinase inhibitor 2B (CDKN2B) gene,
partial cds.
ACCESSION AF058758
VERSION AF058758.1 GI:6808470
KEYWORDS human.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2147)
AUTHORS Murthy,S.K. and Demetrick,D.J.
TITLE Direct Submission
JOURNAL Submitted (09-APR-1998) Pathology and Oncology, University of
Calgary, 3330 Hospital Drive, N.W., Calgary, Alberta T2N 1N4,
Canada
FEATURES Location/Qualifiers
source 1..2147
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/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"
1..>2147
/gene="CDKN2B"
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/codon_start=1
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/protein_id="AAF28397.1"
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/translation="MREENKMPGSGGS"
BASE COUNT 589 a 495 c 512 g 551 t
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Query Match 39.5%; Score 330.4; DB 39; Length 2147;
Best Local Similarity 98.4%; Pred. No. 9.4e-46;
Matches 366; Conservative 0; Mismatches 1; Indels 5; Gaps 3;
QY 1 GAGGACTCGCGCAGC-GTCCGACACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCC 59
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Db 1779 GAGGACTCGCGCAGCGCTCCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCC 1838
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QY 60 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCCCGCTGGTCTTTGAGCGCCAG 119
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Db 1839 GCGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCCCGCTGGTCTTTGAGCGCCAG 1898
|||||
QY 120 AAAGCCCGGAGCTAACGACCGCGCTCGG-CACTGACGGGGCCCCCAAGCGCAGAG 178
|||||
Db 1899 AAAGCCCGGAGCTAACGACCGCGCTCGGCACTGCGCGGCGCCCAAGCGC---AG 1955
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QY 179 AAGGACGCGGAGGCTAATGAAGCTGAGCCCGAGGTCCTCTAGGAGGAGAGAGTCGCGC 238
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Db 1956 AAGGACGCGGAGGCTAATGAAGCTGAGCCCGAGGTCCTCTAGGAGGAGAGAGTCGCGC 2015
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QY 239 GGAGCAGCGTGGGAAGAAAGGAAGAGTCTCGTTAAGTTTACGGCCCAAGCGGTGATTATC 298
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Db 2016 GGAGCAGCGTGGGAAGAAAGGAAGAGTCTCGTTAAGTTTACGGCCCAAGCGGTGATTATC 2075
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QY 299 CGGGCCGCTGCGCGCTCGGGGCTGCGGAATGCGGAGGAGAACAGAGGCATGCCAGTGC 358
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QY 359 GGGGGCGGACGCG 370
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Db 2136 GGGGGCGGACGCG 2147
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Search completed: July 21, 2000, 06:05:24
Job time: 14858 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: July 21, 2000, 06:18:38 ; Search time 107.17 Seconds
(without alignments)
1954.006 Million cell updates/sec

Title: US-09-016-869A-3
Perfect score: 837
Sequence: 1 GAGGACTCCGCGACGGTCCG.....AGGCTGCCAACGGGAGCGG 837

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues
Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	809.6	96.7	850	1 T02963	Cell-cycle regulat
2	677.2	80.9	751	1 T00745	Multiple tumour su
3	677.2	80.9	751	1 Q99165	Human multiple tum
4	677.2	80.9	751	1 T69781	Human multiple tum
5	677.2	80.9	751	1 V11250	Human MTS2 cDNA. D
6	677.2	80.9	751	1 V53831	Coding sequence 2
7	677.2	80.9	751	1 V70595	CDNA encoding a hu
8	360	43.0	1244	1 T00741	Multiple tumour su
9	360	43.0	1244	1 Q99168	Human MTS2 DNA inc
10	360	43.0	1244	1 V11241	Human MTS2 genomic
11	360	43.0	1244	1 V53822	Nucleotide sequenc
12	360	43.0	1244	1 V70586	Human multiple tum
13	276.8	33.1	580	1 T02964	Cell-cycle regulat
14	271.4	32.4	782	1 X26234	Truncated p27/p16
15	271.4	32.4	1073	1 X26232	Truncated p27/p16
16	266.8	31.9	471	1 V11238	Human MTS1 cDNA. D
17	266.8	31.9	471	1 V53819	Nucleotide sequenc
18	266.8	31.9	471	1 V70583	CDNA encoding a hu
19	266.8	31.9	737	1 X26233	Truncated p27/p16
20	266.8	31.9	947	1 T72311	Human multiple tum
21	266.8	31.9	947	1 V11270	Human MTS1 cDNA va
22	266.8	31.9	947	1 V53851	Coding sequence 3
23	266.8	31.9	947	1 T60615	CDNA encoding a hu
24	266.8	31.9	987	1 T60951	Tumour suppressor
25	266.8	31.9	1028	1 X26231	Truncated p27/p16
26	266.8	31.9	1028	1 T74053	CDK inhibitory fus
27	266.8	31.9	1098	1 X26224	Human p16p27 fusio
28	266.8	31.9	1121	1 X26235	Human p16p27 fusio
29	266.8	31.9	1143	1 T74052	CDK inhibitory fus
30	266.8	31.9	1143	1 X26223	Human p16(GS)p27 f
31	265.6	31.7	1420	1 T74051	CDK inhibitory fus
32	265.6	31.7	1420	1 X26220	Human p27-p16 fusi
33	265.4	31.7	393	1 V70624	Mouse multiple tum

34	265.2	31.7	447	1 T00736	Multiple tumour su
35	265.2	31.7	447	1 Q99158	Human multiple tum
36	265.2	31.7	471	1 T69768	Human multiple tum
37	265.2	31.7	471	1 T69769	Human multiple tum
38	265.2	31.7	947	1 T00747	Multiple tumour su
39	265.2	31.7	948	1 O63491	Inhibitor of cycli
40	265.2	31.7	994	1 T02962	Cell-cycle regulat
41	263.6	31.5	447	1 T00749	Multiple tumour su
42	263.6	31.5	447	1 T00750	Multiple tumour su
43	232	27.7	1131	1 T00744	Multiple tumour su
44	232	27.7	1131	1 Q99164	Human MTS polypept
45	232	27.7	1131	1 T69780	Human multiple tum

ALIGNMENTS

RESULT 1					
T02963					
ID	T02963 standard; cDNA; 850 BP.				
AC	T02963;				
DT	01-MAR-1996 (first entry)				
DE	Cell-cycle regulatory protein p15 cDNA.				
KW	Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor;				
KW	CCR; gene therapy; transgenic animal; cancer; cell proliferation;				
KW	ss; ds.				
OS	Homo sapiens.				
FH	Key	Location/Qualifiers			
FT	Key	338..754			
FT	/*tag= a				
PN	W09528483-M1.				
PD	26-OCT-1995.				
PF	14-APR-1995; U04636.				
PR	14-APR-1994; US-227371.				
PR	25-MAY-1994; US-248812.				
PR	14-SEP-1994; US-306511.				
PR	29-NOV-1994; US-346147.				
PA	(COLDB-) COLD SPRING HARBOR LAB.				
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;				
DR	WPI; 95-373798/48.				
DR	P-PSDB; R85117.				
DR	New cell cycle regulating proteins bind to cyclin dependent kinase -				
PT	and related nucleic acids, antibodies etc., used in diagnosis and				
PT	therapy of abnormal cell proliferation, degeneration etc.				
PS	Claim 43; Page 78; 109pp; English.				
CC	CDNA (T02963) coding for the human cell-cycle regulatory (CCR)				
CC	protein p15 (R85117) was identified in immunoprecipitates of				
CC	HeCat cells arrested at the G1 stage and then restimulated with				
CC	transforming growth factor. The isolated cDNA can be used; to				
CC	detect mutations in CCR genes that lead to cell proliferation;				
CC	to breed transgenic animals to study cellular disorders involving				
CC	CCR allele mutation/misexpression; and to correct CCR-deficient				
CC	cells (gene therapy).				
SQ	Sequence 850 BP; 153 A; 261 C; 312 G; 124 T;				

Query Match	96.7%	Score	809.6;	DB	1;	Length	850;
Best Local Similarity	98.6%	Pred.	NO. 4.1e-165;				
Matches	828;	Conservative	0;	Mismatches	9;	Indels	3;
Gaps	1;						
QY	1	GAGGACTCCGCGACGGTCCGACCCCTGCGGCCAGAGCGGGCTTTGAGCTCGGCTGCTCCG	60				
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QY	61	CGTAGGCGCTTTTCCAGAACATCCAGGCGCGCCCTGGTCTTCTTTCGAGCGCCAGGA	120				
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QY	121	AAAGCCGGAGCTAACGACCGCGCTCGGCACTGACGCGGGCCCCAACGCGCAGAGAA	180				
DB	131	AAAGCCGGAGCTAACGACCGCGCTCGGCACTGACGCGGGCCCCAACGCGCAGAGAA	190				
QY	181	GGACGAGGGAGGGTATGATGAGCTGAGCCCGAGGCTCTCTTAGGAGGAGAGAGTGCGCCGG	240				

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Db 191 GCACACGGGGTAATGAGCTAGCCAGGCTCTCTAGGAGGAGAGTAGTGCCTGG 250
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Db 251 AGCAGCTGGGAAAGAGGAGAGTGTCTTAAGTTTACGGCCAAACGGTGGATTATCCG 310
Qy 301 GGCCTCTGGGCTGTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTGGG 360
Db 311 GGCCTCTGGGCTGTGGGGCTGCGGAATGCGGAGGAGAACAAAGGGCATGCCAGTGGG 370
Qy 361 GCGGCACGATGAGGCTGTGCCA---CGCCGGCGGGGAGCTAGTGCAGAGTGCGA 417
Db 371 GCGGCACGATGAGGCTGTGCCAAGCGCGCGGGGAGCTAGTGCAGAGTGCGA 430
Qy 418 CACTCTCTGGGAGCGGGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGCGATC 477
Db 431 CAGCTCTGGAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGATC 490
Qy 478 CAGTCTATGATGGGAGCGCGCGCTGCGGAGTGTCTGCTCTCCAGCGCGGAG 537
Db 491 CAGTCTATGATGGGAGCGCGCGCTGCGGAGTGTCTGCTCTCCAGCGCGGAG 550
Qy 538 CCCAACTCGCAGACCTTGCCTCTCACCGACCGGTGCATGCTGCCGGAGGCG 597
Db 551 CCCAACTCGCAGACCTTGCCTCTCACCGACCGGTGCATGCTGCCGGAGGCG 610
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Db 611 TTCTCTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 670
Qy 658 TGGGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 717
Db 671 TGGGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 730
Qy 718 CTGCGCACAGCCAGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 777
Db 731 CTGCGCACAGCCAGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 790
Qy 778 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGTCCACGGGAGCGG 837
Db 791 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGTCCACGGGAGCGG 850
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RESULT 2

```
T00745
ID T00745 standard; cDNA; 751 BP.
AC T00745;
DT 08-MAY-1996 (first entry).
DE Multiple tumour suppressor 2 (M2S2) gene ORF.
KW Multiple tumour suppressor; M2S2; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; open reading frame; ORF; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT cds 335..751
FT /*tag= a
PN WO9525813-A1.
PD 28-SEP-1995.
PR 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH) UNIV UTAH RES. FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
DR P-PSDB; R81702.
PT Detecting polymorphism associated with cancer pre-disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
```

```
PS Disclosure; Pages 102-103; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (M2S) gene, using gene probes which hybridise to the M2S2
CC gene ORF T00745 (which encodes R81702). The above assay can also be
CC used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia
CC and pancreas, breast and thyroid cancers, etc..
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
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Query Match 80.9%; Score 677.2; DB 1; Length 751;
Best Local Similarity 97.9%; Pred. No. 8.4e-137;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;
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Qy 1 GAGGACTCCGCGAGC-GTCCGACACCTTCCGAGAGAGCGGCTTTAGCTCGGCTGCTTC 59
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Qy 60 GCGTAGTCGCTTTTCCAGAGCAATCCAGGCGCGCGCTGGTCTTTGAGGCGCCAGG 119
Db 69 GCGTAGTCGCTTTTCCAGAGCAATCCAGGCGCGCGCTGGTCTTTGAGGCGCCAGG 128
Qy 120 AAAAGCCCGAGCTAACGACCGCGCTCGG-CACTGCACGGGCGCCCAAGCCGAGAG 178
Db 129 AAAAGCCCGAGCTAACGACCGCGCTCGGCGCTCGGCGCTCGGCGCCCAAGCCG 185
Qy 179 AAGGACGACGGGAGGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGGAGAGTGGCC 238
Db 186 AAGGACGACGGGAGGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGGAGAGTGGCC 245
Qy 239 GGACGACGCTGGGAAAGAAAGAGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 298
Db 246 GGACGACGCTGGGAAAGAAAGAGAGTGTCTTAAGTTTACGCCCAACGGTGGATTATC 305
Qy 299 CGGCGCTGTGCGCTGTGGGGCTGTGGAGTGTGCGAGGAGAACAAAGGATGCCAGTG 358
Db 306 CGGCGCTGTGCGCTGTGGGGCTGTGGAGTGTGCGAGGAGAACAAAGGATGCCAGTG 365
Qy 359 GGGCGCGCAGCGATGAGGGTGTGGCCA---CGCCGCGCGGGGACTAGTGGAGAGGTGC 415
Db 366 GGGCGCGCAGCGATGAGGGTGTGGCCAAGCGCGCGCGGGGACTAGTGGAGAGGTGC 425
Qy 416 GACACTCTGGGAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGCGGA 475
Db 426 GACACTCTGGGAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGCGGA 485
Qy 476 TCCAGGTCTATGATGGGAGCGCGCGCTGTGGGAGCTGCTGCTCTCCACGCGCGG 535
Db 486 TCCAGGTCTATGATGGGAGCGCGCGCTGTGGGAGCTGCTGCTCTCCACGCGCGG 545
Qy 536 AGCCCAACTCGGAGACCTTGCCTACTCTACCGGACCGGTCATGATGCTGCCCGGAGG 595
Db 546 AGCCCAACTCGGAGACCTTGCCTACTCTACCGGACCGGTCATGATGCTGCCCGGAGG 605
Qy 596 GCTTCTCTGACAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 655
Db 606 GCTTCTCTGACAGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 665
Qy 656 CTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 715
Db 666 CTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
Qy 716 ACCTGCGCAGACCCACGGGGGACTGA 741
Db 726 ACCTGCGCAGACCCACGGGGGACTGA 751
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RESULT 3

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Q99165
ID Q99165 standard; cDNA; 751 BP.
AC Q99165;
DT 03-MAY-1996 (first entry)
DE Human multiple tumour suppressor polypeptide, M2S2 encoding cDNA.
```



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Db 69 GCGTAGGCGGTTTTTCCACAGAACAAATCAGGGCGCGCCGCTGGTCTTGTAGCGCCAGG 128
Qy 120 AAAAGCCCGGAGCTAACACCGCGCGCTCGG-CAGTGCACGGGGCCCAAGCCGACAGAG 178
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Db 129 AAAAGCCCGGAGCTAACACCGCGCGCTCGGCACTGCAGGGGCCCAAGCGC---AG 185
Qy 179 AAGGACACGGGAGGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGAGTGCGCC 238
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Db 186 AAGGACACGGGAGGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGAGTGCGCC 245
Qy 239 GGAGCAGCTGGGAAGAGAGAGAGTGCCTTAAGTTTACGCCCAACGGTGGATTATC 298
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Db 246 GGAGCAGCTGGGAAGAGAGAGAGTGCCTTAAGTTTACGCCCAACGGTGGATTATC 305
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    |||||
Db 306 CGGCGCCCTCGCGCTCTGCGGCTGCGGAATGCGGAGGAGAACAGAGGCGATGCCAGTG 365
Qy 359 GGGCGCGCAGGATGAGGGTCTGGCCA---CGCCGGCGGGGAGCTAGTGGAGAGGTGC 415
    |||||
Db 366 GGGCGCGCAGGATGAGGGTCTGGCCAAGCGCGCGCGGAGCTAGTGGAGAGGTGC 425
Qy 416 GACACTCTCTGGGAAGCGCGCGGATGCCCAACGAGTCAACCGCTTTCGGGAGCGCGCA 475
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Db 426 GACAGCTCTCTGGGAAGCGCGCGGATGCCCAACGAGTCAACCGCTTTCGGGAGCGCGCA 485
Qy 476 TCCAGGTCTATGATGGGAGGCGCGCGCTGCGGAGCTGCTGCTCTCCAGCGCGCGG 535
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Db 486 TCCAGGTCTATGATGGGAGGCGCGCGCTGCGGAGCTGCTGCTCTCCAGCGCGCGG 545
Qy 536 AGCCCAACTGCGCAGACCTTGCACACTCTACCCGACCGGTCATGATGCTGCCCGGGAGG 595
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Db 546 AGCCCAACTGCGCAGACCTTGCACACTCTACCCGACCGGTCATGATGCTGCCCGGGAGG 605
Qy 596 GCTTCTGGACACGCTGGTGGTGTGTCACCGGGCGGGCGCGCTGGAGCTGCGCGGATG 655
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Db 606 GCTTCTGGACACGCTGGTGGTGTGTCACCGGGCGGGCGCGCTGGAGCTGCGCGGATG 665
Qy 656 CTGGGGTCTGTCGCGCTGGAGCTTGGCCGAGGAGCGGGGCCACCGCGAGCTTTCAGGCT 715
    |||||
Db 666 CTGGGGTCTGTCGCGCTGGAGCTTGGCCGAGGAGCGGGGCCACCGCGAGCTTTCAGGCT 725
Qy 716 ACCTGCGCAGACCGCGGGGAGCTGA 741
Db 726 ACCTGCGCAGACCGCGGGGAGCTGA 751
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RESULT 8

```
T00741
ID T00741 standard; DNA; 1244 BP.
AC T00741;
DT 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 2 (MTS2) gene exon 2 contg. fragment.
KW Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; exon 2; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT intron 1..273
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FT exon 274..529
    /*tag= b
    /label= exon 2
FT intron 530..1244
    /*tag= c
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FT PN W09525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
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PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
PT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Example 6: Page 96; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to exon 2
CC (T00741) of the MTS2 gene. The above assay can also be used in the
CC diagnosis and prognosis of melanoma, lymphoma, leukaemia and
CC pancreas, breast and thyroid cancers, etc.
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;
Best Local Similarity 100.0%; Pred. NO. 6.2e-69;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 478 CAGGTCATGATGATGGGAGCGCGCGCTGCGGAGCTGCTGCTCCAGCGCGGAG 537
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Db 271 CAGGTCATGATGATGGGAGCGCGCGCTGCGGAGCTGCTGCTCCAGCGCGGAG 330
Qy 538 CCCAACTGCGCAGACCTTGCACACTCTACCCGACCGGTCATGATGCTGCCCGGGAGGC 597
    |||||
Db 331 CCCAACTGCGCAGACCTTGCACACTCTACCCGACCGGTCATGATGCTGCCCGGGAGGC 390
Qy 598 TTCTGTGACACGCTGGTGGTGTGCTGACCGCGCGGGCGGGCTGGAGCTGCGCGGATGCC 657
    |||||
Db 391 TTCTGTGACACGCTGGTGGTGTGCTGACCGCGCGGGCGGGCTGGAGCTGCGCGGATGCC 450
Qy 658 TGGGTCGCTGCTGCCCTGGAGCTTGGCCGAGGAGCGGGCCACCGAGCTTGCAGGGTAC 717
    |||||
Db 451 TGGGTCGCTGCTGCCCTGGAGCTTGGCCGAGGAGCGGGCCACCGAGCTTGCAGGGTAC 510
Qy 718 CTGGCAGCAGCCAGGGGAGCTGACGCCAGGTTCCCGAGCGCGCCACAGACTTTATTT 777
    |||||
Db 511 CTGGCAGCAGCCAGGGGAGCTGACGCCAGGTTCCCGAGCGCGCCACAGACTTTATTT 570
Qy 778 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGGCTGCCACGGGGAGCGG 837
    |||||
Db 571 TCTTACCAATTTCCACCCACCCACCTAATTCGATGAAGGCTGCCACGGGGAGCGG 630

RESULT 9
Q99168
ID Q99168 standard; cDNA; 1244 BP.
AC Q99168;
DT 07-MAY-1996 (first entry)
DE Human MTS2 DNA including exon 2, intron 2 and part of intron 1.
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW gene therapy; chronic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT intron 1..273
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    /number= 1
FT exon 274..580
    /*tag= b
    /number= 1
FT intron 581..1244
    /*tag= c
    /number= 2
FT PN W09525429-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03316.
PR 18-MAR-1994; US-214581.
PR 18-MAR-1994; US-214582.
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PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215088.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 95-344401/44.
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
PS Example 6: Page 96; 156pp; English.
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC polypeptides have been isolated and sequenced. This sequence includes
CC intron 2, exon 2 and part of intron 1 of the MTS polypeptide, MTS2. MTS
CC polypeptide-encoding cDNAs and mutants of these are useful for the
CC diagnosis or prognosis of human cancer. Germ-line mutations of MTS
CC cDNAs can be used for diagnosing predisposition to melanoma, leukaemia,
CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL
CC and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney,
CC stomach and rectum. The wild-type gene is useful for gene therapy and
CC MTS polypeptides may also be used for protein replacement therapy. Also
CC the polypeptides or cells contg. an altered MTS gene are useful for
CC screening for potential cancer therapeutics.
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;
Best Local Similarity 100.0%; Pred. No. 6.2e-69;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 537
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DB 271 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 330
QY 538 CCCAACTGCGAGACCTGCCACTCTCACCCGACGGTGCATGATGCTGCCGGGAGGCG 597
|||||
DB 331 CCCAACTGCGAGACCTGCCACTCTCACCCGACGGTGCATGATGCTGCCGGGAGGCG 390
QY 598 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657
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DB 391 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 450
QY 658 TGGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCAAGGTAC 717
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DB 451 TGGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCAAGGTAC 510
QY 718 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCCCGACCGCCCAACGACTTTATTT 777
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DB 511 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCCCGACCGCCCAACGACTTTATTT 570
QY 778 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837
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DB 571 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630

RESULT 10
V11241
ID V11241 standard; DNA; 1244 BP.
AC V11241;
DT 15-JUL-1998 (first entry)
DE Human MTS2 genomic DNA including exon 2.
KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Intron 1..273
FT /*tag= a
FT /number= 1
FT exon 274..529
FT /*tag= b
FT /number= 2
FT /note= "Corresponds to exon 2 in V11240"

PN US5739027-A.
PD 14-APR-1998.
PR 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-U03316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 98-250421/22.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PS Disclosure: Fig 7; 72pp; English.
CC This sequence encodes the human multiple tumour suppression protein,
CC MTS1, exon 2. The MTS gene locus is also referred to as the familial
CC melanoma (FML) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;

Query Match 43.0%; Score 360; DB 1; Length 1244;
Best Local Similarity 100.0%; Pred. No. 6.2e-69;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 478 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 537
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DB 271 CAGGTCATGATGAGGAGCGCCCGCTGGCGGAGCTGCTGCTCCACGGCGGGAG 330
QY 538 CCCAACTGCGAGACCTGCCACTCTCACCCGACGGTGCATGATGCTGCCGGGAGGCG 597
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DB 331 CCCAACTGCGAGACCTGCCACTCTCACCCGACGGTGCATGATGCTGCCGGGAGGCG 390
QY 598 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657
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DB 391 TTCCTGGACACGCTGGTGTGCTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 450
QY 658 TGGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCAAGGTAC 717
|||||
DB 451 TGGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCACGTTGCAAGGTAC 510
QY 718 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCCCGACCGCCCAACGACTTTATTT 777
|||||
DB 511 CTGCGCACAGCCACGGGGAGCTGACCCAGGTTCCCGACCGCCCAACGACTTTATTT 570
QY 778 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 837
|||||
DB 571 TCTTACCAATTTCCACCGCCACCCACCTAATTCGATGAAGGCTGCCAACGGGAGCGG 630

RESULT 11
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ID V53822 standard; cDNA; 1244 BP.
AC V53822;
DT 04-DEC-1998 (first entry)
DE Nucleotide sequence of the multiple tumour suppressor 2.
KW Multiple tumour suppressor 2; MTS-2; human; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Intron 1..273
FT /*tag= a
FT /note= "intron 1"
FT US5801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.

KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated; ss.
OS Homo sapiens.
EN W09906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
PT fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60: Page 83-84; 88pp; English.

Search completed: July 21, 2000, 06:18:48
Job time: 13645 sec

CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/pl6 fusion
CC protein.
SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

Query Match 32.48; Score 271.4; DB 1; Length 1073;
Best Local Similarity 77.6%; Pred. No. 5.5e-50;
Matches 342; Conservative 0; Mismatches 96; Indels 3; Gaps 1;
QY 301 GGCCGCTCGGCTGTGGGGCTGCGGAATGCGGAGGAGAACAAAGGCGATGCCCGAGTGGG 360
DB 562 GGGGTGCGGTTCCGGCGGGGTGGATCCGTCAGAGATCCGGCGGGGAGGAGCATG 621
QY 361 GGCGGACGATGAGGGTCTGGCCACG---CCGGCGGGGAGCTAGTGAGAGGTCGA 417
DB 622 GAGCCTTCGGCTGACTGCTGGCCACGCGCGCGGGGTGCGGTAGAGGAGTCCGG 681
QY 418 CACTCTGGGAAGCGGGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGGCGCGCATC 477
DB 682 GCGCTGTGGAGGGGGGGCGCTGCCCAACACACCGAATAGTTACGTCGGAGGCCGATC 741
QY 478 CAGGTCATGATGATGGGCGAGCGCGCGTGGCGGAGTGTGCTGCTCCACGCGCGGAG 537
DB 742 CAGGTCATGATGATGGGCGAGCGCGCGAGTGGCGGAGTGTGCTGCTCCACGCGCGGAG 801
QY 538 CCCAACTCCGACACCCCTGCCACTCTCACCCGACCGGTGTCATGATGCTGCCGGGAGGCG 597
DB 802 CCCAACTCCGCGCGACCCCGCACCTCTCACCCGACCGGTGTCACGACGCTGCCGGGAGGCG 861
QY 598 TTCCTGGACACGCTGGTGGTGTGCTGACCGGGCGGGGGCGGGTGGAGCTGCCGGATGCC 657
DB 862 TTCCTGGACACGCTGGTGGTGTGCTGACCGGGCGGGGGCGGGTGGAGCTGCCGGATGCC 921
QY 658 TGGGTGCTGTGCCCGTGGACTTGGCGGAGGAGCGGGGCCACCGCGACGTTGACGGGTAC 717
DB 922 TGGGGCCGCTGTGCCCGTGGACTTGGCGGAGGAGTGGGCCATCCCGATGTCGCACGCTAC 981
QY 718 CTGGCACACGACCGGGGGAC 738
DB 982 CTGGCGCGGCTGCGGGGGC 1002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:06:23 ; Search time 86.37 Seconds
(without alignments)
1333.035 Million cell updates/sec

Title: US-09-016-869A-3
Perfect score: 837
Sequence: 1 GAGGACGCCGACGTCGCG.....AGGCTGCCACGGGACGG 837

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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2: /cgn2_6/ptodata/1/lna/5B_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	837	100.0	837	4	US-08-306-511A-3
2	837	100.0	837	4	US-08-893-274-3
3	812.8	97.1	850	4	US-08-627-610-3
4	812.8	97.1	850	5	US-08-581-918A-3
5	812.8	97.1	850	6	PCT-US95-04636-3
6	677.2	80.9	751	1	US-08-474-177-15
7	677.2	80.9	751	2	US-08-487-033-15
8	677.2	80.9	751	3	US-08-480-810-15
9	677.2	80.9	751	3	US-08-508-735-15
10	677.2	80.9	751	4	US-08-848-251-15
11	677.2	80.9	751	4	US-08-486-047-15
12	677.2	80.9	751	5	US-09-120-130-15
13	677.2	80.9	751	5	US-09-115-252-15
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22	276.8	33.1	580	4	US-08-627-610-7
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25	266.8	31.9	471	1	US-08-474-177-1
26	266.8	31.9	471	2	US-08-487-033-1

27	266.8	31.9	471	2	US-08-480-810-1	Sequence 1, Appli
28	266.8	31.9	471	3	US-08-508-735-1	Sequence 1, Appli
29	266.8	31.9	471	4	US-08-848-251-1	Sequence 1, Appli
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32	266.8	31.9	471	5	US-09-115-252-1	Sequence 1, Appli
33	266.8	31.9	947	1	US-08-474-177-36	Sequence 36, Appl
34	266.8	31.9	947	2	US-08-487-033-36	Sequence 36, Appl
35	266.8	31.9	947	2	US-08-480-810-36	Sequence 36, Appl
36	266.8	31.9	947	3	US-08-508-735-36	Sequence 36, Appl
37	266.8	31.9	947	4	US-08-848-251-36	Sequence 36, Appl
38	266.8	31.9	947	4	US-08-486-047-36	Sequence 36, Appl
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42	265.4	31.7	393	3	US-08-508-735-45	Sequence 45, Appl
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45	265.2	31.7	994	4	US-08-627-610-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-306-511A-3
; Sequence 3, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 328..738
US-08-306-511A-3

Query Match 100.0%; Score 837; DB 4; Length 837;
Best Local Similarity 100.0%; Pred. No. 3.4e-179;

Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGACTCCGCGAGGTCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCCG 60
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Qy 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGCTTCTTGGCGCCAGGA 120
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Qy 121 AAAGCCGAGCTAACGACCGCGCTCGGCACCTGCGGCGCCCAAGCGCCAGAGAA 180
Db 121 AAAGCCGAGCTAACGACCGCGCTCGGCACCTGCGGCGCCCAAGCGCCAGAGAA 180

Qy 181 GGACGACGGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTCCGCCGG 240
Db 181 GGACGACGGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTCCGCCGG 240

Qy 241 AGCAGCTGGGAAAGAGGGAAGAGTGTCTTAAGTTAGCGCCCAAGCGTGGATTATCCG 300
Db 241 AGCAGCTGGGAAAGAGGGAAGAGTGTCTTAAGTTAGCGCCCAAGCGTGGATTATCCG 300

Qy 301 GCGCGCTCGGCTTGGGGCTCGGGAATGCGGAGGAGAACAGGCGATGCCAGTGGG 360
Db 301 GCGCGCTCGGCTTGGGGCTCGGGAATGCGGAGGAGAACAGGCGATGCCAGTGGG 360

Qy 361 GCGCGCAGCATGAGGCTTGGCCACCGCGCGCGGAGCTAGTGGAGAAAGTGGCAGAC 420
Db 361 GCGCGCAGCATGAGGCTTGGCCACCGCGCGCGGAGCTAGTGGAGAAAGTGGCAGAC 420

Qy 421 TCCTGGGAGCGCGCGGATCCCAAGGAGTCAACCGTTTCGGGAGCGCGGATCCAG 480
Db 421 TCCTGGGAGCGCGCGGATCCCAAGGAGTCAACCGTTTCGGGAGCGCGGATCCAG 480

Qy 481 GTCATGATGAGGCGCGCGGCTGCGGAGCTGCTGCTGCCACGCGCGGAGCGCC 540
Db 481 GTCATGATGAGGCGCGCGGCTGCGGAGCTGCTGCTGCCACGCGCGGAGCGCC 540

Qy 541 AACTGCGCAGACCTGCGACCTCTCACCGCAGCGGTGATGATGCTGCCGGAGGCTTC 600
Db 541 AACTGCGCAGACCTGCGACCTCTCACCGCAGCGGTGATGATGCTGCCGGAGGCTTC 600

Qy 601 CTGGACAGCTGTGTGCTGCTCACCGCGCGGCGGCGGCTGGACGTGCGGATGCTGG 660
Db 601 CTGGACAGCTGTGTGCTGCTCACCGCGCGGCGGCGGCTGGACGTGCGGATGCTGG 660

Qy 661 GGTGCTGTGCGCGTGGACTTGGCGAGGAGCGGGCGCCACGCGACGTTCGAGGCTACCTG 720
Db 661 GGTGCTGTGCGCGTGGACTTGGCGAGGAGCGGGCGCCACGCGACGTTCGAGGCTACCTG 720

Qy 721 CGCAGCGCAGGGGAGCTGACGCCAGGTTCCCGAGCGCCCGCCACAGGACTTTATTTCT 780
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Qy 781 TACCCAAATTTCCACCCCGCCACCTTAATTCGATGAGCTGCCACGCGGAGCGG 837
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RESULT 2
US-08-93-274-3
; Sequence 3, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
NAME/KEY: CDS
LOCATION: 328..738
US-08-893-274-3

Query Match 100.0%; Score 837; DB 4; Length 837;
Best Local Similarity 100.0%; Pred. No. 3 4e-179;
Matches 837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGACTCCGCGAGGTCGCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCCG 60
Db 1 GAGGACTCCGCGAGGTCGCGACCCCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTTCCG 60

Qy 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGCTTCTTGGCGCCAGGA 120
Db 61 CGCTAGGCGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGCTTCTTGGCGCCAGGA 120

Qy 121 AAAGCCGAGCTAACGACCGCGCTCGGCACCTGCGGCGCCCAAGCGCCAGAGAA 180
Db 121 AAAGCCGAGCTAACGACCGCGCTCGGCACCTGCGGCGCCCAAGCGCCAGAGAA 180

Qy 181 GGACGACGGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTCCGCCGG 240
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Qy 241 AGCAGCTGGGAAAGAGGGAAGAGTGTCTTAAGTTAGCGCCCAAGCGTGGATTATCCG 300

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Db 241 AGCAGCGTGGGAAGGAGGAGTGTCTTAAGTTTACGGCCACAGGTGGATTATCCG 300
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Db 301 GCGCGTGGCGCTCTGGGGCTCGGAATCGCGAGGAGAACAAAGGCGATGCCAGTGGG 360
QY 361 GCGCGCAGGATGAGGTCTGGCCAGCGCGCGCGCGGGGACTAGTGAGAGGTGGCACAC 420
Db 361 GCGCGCAGGATGAGGTCTGGCCAGCGCGCGCGCGGGGACTAGTGAGAGGTGGCACAC 420
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Db 421 TCTGTGGAAGCGCGCGGATCCACGAGTCAACGTTTTCGGGAGGCGCGGATCCAG 480
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Db 481 GTCATGATGATGGGACGCGCGCGCGTGGCGAGTCTGTGTCTCCACGCGCGGAGCCC 540
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Db 541 AACTGCGAGACCCCTGCCACTCTACCCGACCGGTGATGATGCTGCCCGGAGGCGTTC 600
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QY 781 TACCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837
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RESULT 3
US-08-627-610-3
; Sequence 3, Application US/08627610
; Patent No. 5919997
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Serrano, Manuel
; APPLICANT: Depinho, Ronald A.
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
; TITLE OF INVENTION: Regulation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 338..751
US-08-627-610-3

Query Match 97.1%; Score 812.8; DB 4; Length 850;
Best Local Similarity 98.8%; Pred. No. 8.e-174;
Matches 830; Conservative 0; Mismatches 7; Indels 3; Gaps 1;

QY 1 GAGGACTCGCGACGGTCCGCCACCTTGCAGCGCCAGAGCGGCTTTGAGCTCGGCTTCCG 60
Db 11 GAGGACTCGCGACGGTCCGCCACCTTGCAGCGCCAGAGCGGCTTTGAGCTCGGCTTCCG 70
QY 61 CGCTAGCGGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGGTCTTTGAGCGCCAGGA 120
Db 71 CGCTAGCGGCTTTTCCAGAAAGCAATCCAGGCGCGCGCTGGTCTTTGAGCGCCAGGA 130
QY 121 AAAGCCCGGAGTAAAGCAGCGCGCTCGGCACCTGACGCGGCGCCCAAGCCGAGAGAA 180
Db 131 AAAGCCCGGAGTAAAGCAGCGCGCTCGGCACCTGACGCGGCGCCCAAGCCGAGAGAA 190
QY 181 GGACGACGGAGGGTAAATGAAGCTGAGCGCCAGGTCTCTAGGAGGAGAGAGTGCAGG 240
Db 191 GGACGACGGAGGGTAAATGAAGCTGAGCGCCAGGTCTCTAGGAGGAGAGAGTGCAGG 250
QY 241 AGCAGCGTGGGAAAGGAGAGTGTCTTAAGTTTACGGCCACGCGTGGATTATCCG 300
Db 251 AGCAGCGTGGGAAAGGAGAGTGTCTTAAGTTTACGGCCACGCGTGGATTATCCG 310
QY 301 GCGCGTGCCTCTTGGGGCTCGGGAATGCGGAGGAGAACAAAGGCGCATGCCAGTGGG 360
Db 311 GCGCGTGCCTCTTGGGGCTCGGGAATGCGGAGGAGAACAAAGGCGCATGCCAGTGGG 370
QY 361 GCGCGCAGCATGAGGTCTGGCCA--CGCCGCGCGGGGACTAGTGAGAGGTGCGGA 417
Db 371 GCGCGCAGCATGAGGTCTGGCCAAGCGCGCGGGGACTAGTGAGAGGTGCGGA 430
QY 418 CACTCTGGGAAAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGATC 477
Db 431 CAGCTCTGGAGCGCGCGGATCCCAACGAGTCAACCGTTTCGGGAGCGCGGATC 490
QY 478 GAGGTGATGATGGGACGCGCGCGTGGGGAGCTGCTGCTGCCAGCGCGGAG 537
Db 491 GAGGTGATGATGGGACGCGCGCGTGGGGAGCTGCTGCTGCCAGCGCGGAG 550
QY 538 CCAACTGCGAGACCTTCCACTCTCACCGACCGGTGCATGATGCTGCCCGGGAGGC 597
Db 551 CCAACTGCGAGACCTTCCACTCTCACCGACCGGTGCATGATGCTGCCCGGGAGGC 610
QY 598 TTCTTGACACGCTGTGTGTGTGACACCGCGCGCGGCTGGACGTGCCGATGCC 657
Db 611 TTCTTGACACGCTGTGTGTGTGACACCGCGCGGCTGGACGTGCCGATGCC 670
QY 658 TGGGTGCTGTGCGCGTGGACTTGGCCGAGGAGCGGGGACCGCACGCTTGACGGGTAC 717
Db 671 TGGGTGCTGTGCGCGTGGACTTGGCCGAGGAGCGGGGACCGCACGCTTGACGGGTAC 730
QY 718 CTGCGCAGACCCACGCGGACTGACCCAGGTTCGCCAGCGCCCAACGACTTTATT 777
Db 731 CTGCGCAGACCCACGCGGACTGACCCAGGTTCGCCAGCGCCCAACGACTTTATT 790
QY 778 TCTTACCCCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 837
Db 791 TCTTACCCCAATTTCCACCCACCCACCTAATTCGATGAAGCTGCCAACGGGAGCGG 850

APPLICATION NUMBER: PCT/US95/04636
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 338..751
PCT-US95-04636-3

Query Match 97.1%; Score 812.8; DB 6; Length 850;
Best Local Similarity 98.8%; Pred. No. 8.8e-174;
Matches 830; Conservative 0; Mismatches 7; Indels 3; Gaps 1;
QY 1 GAGGACTCGCGACGCTCGCCACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCGG 60
DB 11 GAGGACTCGCGACGCTCGCCACCTCGCGCCAGAGCGGCTTTGAGCTCGGCTGCTCGG 70
QY 61 CGCTAGGCGCTTTTCCAGAGAGCAATCAGCGCGCGCGCTGGTCTTGGAGCGCCAGGA 120
DB 71 CGCTAGGCGCTTTTCCAGAGAGCAATCAGCGCGCGCGCTGGTCTTGGAGCGCCAGGA 130
QY 121 AAAGCCGGAGCTAACGACCGCGCTCGGCACTGACGCGGCGCCCAAGCCGAGAGAA 180
DB 131 AAAGCCGGAGCTAACGACCGCGCTCGGCACTGACGCGGCGCCCAAGCCGAGAGAA 190
QY 181 GGACGACGGAGGTTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGCCCGGG 240
DB 191 GGACGACGGAGGTTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGCCCGGG 250
QY 241 AGCAGCGTGGGAAGAGGAGAGTGTCTTAAGTTTACGGCCACGCTGGATTATCCG 300
DB 251 AGCAGCGTGGGAAGAGGAGAGTGTCTTAAGTTTACGGCCACGCTGGATTATCCG 310
QY 301 GCGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAAAGGGCATGCCAGTGGG 360
DB 311 GCGCGCTGCGCGTCTGGGGCTGCGGAATGCGGAGGAGAAAGGGCATGCCAGTGGG 370
QY 361 GCGCGCAGCGATGAGGCTGTGCGCA---CGCCGCGCGGGAGTACTGGAGAGAGTGCGA 417
DB 371 GCGCGCAGCGATGAGGCTGTGCGCAAGCGCGCGCGGGGACTAGTGAGAGAGTGCGCA 430
QY 418 CACTCTGGAGACCGCGCGGATCCACAGGAGTCAACGGTTTCGGGAGGCGCGCGATC 477
DB 431 CAGCTCTGGAGACCGCGCGGATCCACAGGAGTCAACGGTTTCGGGAGGCGCGCGATC 490
QY 478 CAGGTATGATGATGGCAGCGCGCGCTGGCGGAGCTGCTGCTGCTCCACGCGCGGAG 537
DB 491 CAGGTATGATGATGGCAGCGCGCGCTGGCGGAGCTGCTGCTGCTCCACGCGCGGAG 550
QY 538 CCCAACTGGCGACACCTGCGCACTCTCACCCGACCGGTGATGATGCTGCCCGGGAGGGC 597
DB 551 CCCAACTGGCGACACCTGCGCACTCTCACCCGACCGGTGATGATGCTGCCCGGGAGGC 610
QY 598 TTCCTGGACACGCTGTGTGTGCTGCTACCGGGCGCGCGCTGGAGAGTGCCTGATGCC 657

DB 611 TTCCTGGACACGCTGTGTGTGCTGACCGGGCGCGGCTGGACGTGCGCATGCC 670
QY 658 TGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGAGCTTTCGAGGGTAC 717
DB 671 TGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGGAGCTTTCGAGGGTAC 730
QY 718 CTGCCACAGCCACGGGGAGTGGCCAGGTTCCCGAGCCGCCACACAGACTTTATTT 777
DB 731 CTGCCACAGCCACGGGGAGTGGCCAGGTTCCCGAGCCGCCACACAGACTTTATTT 790
QY 778 TCTTACCAATTTCCACCCACCCCACTAATTCGATGAAGCTGCCAACGGGAGGG 837
DB 791 TCTTACCAATTTCCACCCACCCCACTAATTCGATGAAGCTGCCAACGGGAGGG 850
RESULT 6
US-08-474-177-15
Sequence 15, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474.177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 335..751
US-08-474-177-15

Query Match 80.9%; Score 677.2; DB 1; Length 751;
Best Local Similarity 97.9%; Pred. No. 1.8e-143;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 GAGGACTCCGGGAGG-GTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 59
Db 9 GAGGACTCCGGGAGGCTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 68

Qy 60 GCGCTAGGCGCTTTTCCAGAACCAATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 119
Db 69 GCGCTAGGCGCTTTTCCAGAACCAATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 128

Qy 120 AAAAGCCGGAGCTAAGCAGCGCGCTCGG-CACTGACGGGCGCCCAAGCCGAGAG 178
Db 129 AAAAGCCGGAGCTAAGCAGCGCGCTCGGCACTGACGGGCGCCCAAGCCG---AG 185

Qy 179 AAGGACGAGCGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTGCGCC 238
Db 186 AAGGACGAGCGGAGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGTGCGCC 245

Qy 239 GGAGCAGGCTGGGAAGAAGGAAGAGTGTCTTAAGTTTACGGCCACCGTGGATTATC 298
Db 246 GGAGCAGGCTGGGAAGAAGGAAGAGTGTCTTAAGTTTACGGCCAAACGTTGGATTATC 305

Qy 299 CGGCGCGCTGCGCTCTGGGGCTGCGGAATGCGGAGGAGACAGAGGCGATGCCAGTG 358
Db 306 CGGCGCGCTGCGCTCTGGGGCTGCGGAATGCGGAGGAGACAGAGGCGATGCCAGTG 365

Qy 359 GGGGCGGCGAGGATGAGGCTGTGGCCA---CGCGCGCGGGGAGTGTGAGGAAGGTGC 415
Db 366 GGGGCGGCGAGGATGAGGCTGTGGCCAAGCGCGCGCGGGGAGTGTGAGGAAGGTGC 425

Qy 416 GACACTCTGGGAAGCGCGCGGATCCCAAGGAGTCAACCGTTTCGGGAGCGCGCGA 475
Db 426 GACAGCTCTGGGAAGCGCGCGGATCCCAAGGAGTCAACCGTTTCGGGAGCGCGCGA 485

Qy 476 TCCAGGTCATGATGATGGCAGCGCGCGCTGCGGAGCTGCTCTCCACGCGCGG 535
Db 486 TCCAGGTCATGATGATGGCAGCGCGCGCTGCGGAGCTGCTCTCCACGCGCGG 545

Qy 536 AGCCCAACTGCGCAGACCTGCCACTCTACCCGACCGGTGCATGATGCTGCCGCGGAGG 595
Db 546 AGCCCAACTGCGCAGACCTGCCACTCTACCCGACCGGTGCATGATGCTGCCGCGGAGG 605

Qy 596 GCTTCTGGACACCGCTGGTGTGTCACCGCGCGCGCGCGCGGCTGGAGTCCGCGATG 655
Db 606 GCTTCTGGACACCGCTGGTGTGTCACCGCGCGCGCGCGGCTGGAGTCCGCGATG 665

Qy 656 CCGGGTGTCTGCGCGTGGCTTGGCGAGGAGCGGCGCCACCGGAGCTTGCAGGCT 715
Db 666 CCGGGTGTCTGCGCGTGGCTTGGCGAGGAGCGGCGCGCCACCGGAGCTTGCAGGCT 725

Qy 716 ACCTGCGCAGACCGCGGGGAGCTGA 741
Db 726 ACCTGCGCAGACCGCGGGGAGCTGA 751

RESULT 7

us-08-487-033-15
; Sequence 15, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:

APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 335..751
US-08-487-033-15

Query Match 80.9%; Score 677.2; DB 2; Length 751;
Best Local Similarity 97.9%; Pred. No. 1.8e-143;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

Qy 1 GAGGACTCCGGGAGG-GTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 59
Db 9 GAGGACTCCGGGAGGCTCCGCAACCCCTGCGGCCAGAGCGGCTTTGAGCTCGGTGCTTCC 68

Qy 60 GCGCTAGGCGCTTTTCCAGAACCAATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 119
Db 69 GCGCTAGGCGCTTTTCCAGAACCAATCCAGGCGCGCCGCTGGTTCCTTGAGCGCCAGG 128

QY 120 AAAAGCCGGAGCTAACGACCGCGCGCTCGG-CAGTCACGGGGCCCCCAAGCCCAAG 178
Db 129 AAAAGCCGGAGCTAACGACCGCGCGCTCGGCACTCAGCGGGCCCCCAAGCCGC--AG 185
QY 179 AAGGACACGGGAGGTAATGAAGCTGAGCCAGGTCTCTAGGAAGAGAGTGGCC 238
Db 186 AAGGACACGGGAGGTAATGAAGCTGAGCCAGGTCTCTAGGAAGAGAGTGGCC 245
QY 239 GGAGACGCTGGGAAAGAGGAGAGTGTCTTAAAGTTACGCCCAACGGTGGATTATC 298
Db 246 GGAGACGCTGGGAAAGAGGAGAGTGTCTTAAAGTTACGCCCAACGGTGGATTATC 305
QY 299 CGGGCCCTCGCGCTCGGGGCTGCGGATGCGGAGGAGAACAGGGATGCCAGTG 358
Db 306 CGGGCCCTCGCGCTCGGGGCTGCGGATGCGGAGGAGAACAGGGATGCCAGTG 365
QY 359 GGGCGGCAGCGATGAGGGTCTTGCCCA--CGCCGGCGGGGACTAGTGAGAGTGC 415
Db 366 GGGCGGCAGCGATGAGGGTCTTGCCAGCGCGCGGGGACTAGTGAGAGTGC 425
QY 416 GACACTCTGGGAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCGA 475
Db 426 GACAGTCTCTGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCGA 485
QY 476 TCCAGGTCTGATGATGGGAGCGCGCGCGCTGGCGGAGTCTGCTCTCCACGGCGCG 535
Db 486 TCCAGGTCTGATGATGGGAGCGCGCGCGCTGGCGGAGTCTGCTCTCCACGGCGCG 545
QY 536 AGCCCAACTGCGAGACCTTGCACCTCTCACCCGCGGCTGATGATGCTGCCGGGAGG 595
Db 546 AGCCCAACTGCGAGACCTTGCACCTCTCACCCGCGGCTGATGATGCTGCCGGGAGG 605
QY 596 GCTTCTGGACACGCTGCTGCTGCTGACCGCGCGCGCGCGCGCTGACGTGCGCGATG 655
Db 606 GCTTCTGGACACGCTGCTGCTGCTGACCGCGCGCGCGCGCGCTGACGTGCGCGATG 665
QY 656 CTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
Db 666 CTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 725
QY 716 ACTGCGCACAGCCACCGGGGACTGA 741
Db 726 ACTGCGCACAGCCACCGGGGACTGA 751

RESULT 8

US-08-480-810-15
; Sequence 15, Application US/08480810
; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Beutler, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
; US-08-480-810-15

Query Match 80.9%; Score 677.2; DB 2; Length 751;

Best Local Similarity 97.9%; Pred. No. 1.8e-143;

Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

QY 1 GAGGACTCCGCGAGG-GTCCGACACCTTCGCGCCAGAGCGGCTTTGAGCTGGCTGCTTCC 59

Db 9 GAGGACTCCGCGAGGCTCCGACCTTCGCGCCAGAGCGGCTTTGAGCTGGCTGCTTCC 68

QY 60 GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG 119

Db 69 GCCTAGGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTGGTCTTTGAGCGCCAGG 128

QY 120 AAAAGCCCGGAGCTAACGACCGCGCGCTCGG-CAGTCACGGGGCCCCCAAGCCCAAG 178

Db 129 AAAAGCCCGGAGCTAACGACCGCGCGCTCGGCACTCAGCGGGCCCCCAAGCCGC--AG 185

QY 179 AAGGACACGGGAGGTAATGAAGCTGAGCCAGGTCTCTAGGAAGAGAGTGGCC 238

Db 186 AAGGACACGGGAGGTAATGAAGCTGAGCCAGGTCTCTAGGAAGAGAGTGGCC 245

QY 239 GGAGACGCTGGGAAAGAGGAGTGTCTTAAAGTTACGCCCAACGGTGGATTATC 298

Db 246 GGAGACGCTGGGAAAGAGGAGTGTCTTAAAGTTACGCCCAACGGTGGATTATC 305

QY 299 CGGGCCCTCGCGCTTCGGGGCTGCGGATGCGGAGGAGAACAGGGATGCCAGTG 358

Db 306 CGGGCCCTCGCGCTTCGGGGCTGCGGATGCGGAGGAGAACAGGGATGCCAGTG 365

QY 359 GGGCGGCAGCGATGAGGGTCTTGCCCA--CGCCGGCGCGGGGACTAGTGAGAGTGC 415

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QY 416 GACACTCTGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCGA 475

Db 426 GACACTCTGGAAGCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCGA 485

QY 476 TCCAGGTGATGATGGGACGCGCCCGGTGGCGGAGCTGCTGCTCCACGCGCGG 535
Db 486 TCCAGGTGATGATGGGACGCGCCCGGTGGCGGAGCTGCTGCTCCACGCGCGG 545
QY 536 AGCCCAACTGGCAGACCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGAGG 595
Db 546 AGCCCAACTGGCAGACCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGAGG 605
QY 596 GCTTCTTGACACGCTGGTGTGCTGCACCGCGCGCGCGGTGGACGTGCGCGATG 655
Db 606 GCTTCTTGACACGCTGGTGTGCTGCACCGCGCGCGGTGGACGTGCGCGATG 665
QY 656 CTTGGGGTGTGCTGCGCGGTGGCGGAGGACCGCGCGCGGTGGCGGAGGTTGCGAGGT 715
Db 666 CTTGGGGTGTGCTGCGCGGTGGCGGAGGACCGCGCGCGGTGGCGGAGGTTGCGAGGT 725
QY 716 ACTTGGCAGACCGCGCGGAGTGA 741
Db 726 ACTTGGCAGACCGCGCGGAGTGA 751

RESULT 9
US-08-508-735-15
; Sequence 15, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MPS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens.
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 335..751
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 490..491
; OTHER INFORMATION: /note= "Splice site"
US-08-508-735-15

Query Match 80.9%; Score 677.2; DB 3; Length 751;
Best Local Similarity 97.9%; Pred. No. 1.8e-143;
Matches 730; Conservative 0; Mismatches 8; Indels 8; Gaps 4;

QY 1 GAGGACTCCGCGAGCG -GTCCGCAACCCCTGCGGCCACAGAGCGGCTTTTGTAGCTCGGCTGCTTCC 59
Db 9 GAGGACTCCGCGAGCGCTCCGCAACCCCTGCGGCCACAGAGCGGCTTTTGTAGCTCGGCTGCTTCC 68
QY 60 GCGGTAGCGCGCTTTTCCCAAGCAATCCAGAGCGCGCCGCTGCTTCTTGTAGCGCGCAGG 119
Db 69 GCGGTAGCGCGCTTTTCCCAAGCAATCCAGAGCGCGCCGCTGCTTCTTGTAGCGCGCAGG 128
QY 120 AAAAGCCCGGAGCTAAGCAGCCGCGCTCGG -CACTGCACGCGCGCCCAAGCCGACAGAG 178
Db 129 AAAAGCCCGGAGCTAAGCAGCCGCGCTCGGCACTGCACGCGCGCCCAAGCCGACAGAG 185
QY 179 AAGGACGACGGGAGGTTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGGCC 238
Db 186 AAGGACGACGGGAGGTTAATGAAGCTGAGCCAGCTCTCTAGGAAGAGAGAGTGGCC 245
QY 239 GGAGCAGCGTGGGAAAGAGGAGAGTGTGTTAAGTTTACGCCCAACGCTGATATTC 298
Db 246 GGAGCAGCGTGGGAAAGAGGAGAGTGTGTTAAGTTTACGCCCAACGCTGATATTC 305
QY 299 CGGCGCGCTGCGCTCTGGGGGCTGCGGAATCGCGAGGAGAACAAAGGCAATGCCAGTG 358
Db 306 CGGCGCGCTGCGCTCTGGGGGCTGCGGAATCGCGAGGAGAACAAAGGCAATGCCAGTG 365
QY 359 GGGCGGCGAGCGATGAGGCTTGCCCA ---CGCGCGCGCGGGGACTAGTGAGAGGTC 415
Db 366 GGGCGGCGAGCGATGAGGCTTGCCCAAGCGCGCGCGGGGACTAGTGAGAGGTC 425
QY 416 GACACTCTGGGAAGCGCGCGGATCCCAACGAGGATCAACCGTTTCGGGAGGCGCGGA 475
Db 426 GACAGCTCTGGGAAGCGCGCGGATCCCAACGAGGATCAACCGTTTCGGGAGGCGCGGA 485
QY 476 TCCAGGTGATGATGGCAGCGCCCGCGTGGCGGAGCTGCTGCTCCACGCGCGG 535
Db 486 TCCAGGTGATGATGGCAGCGCCCGCGTGGCGGAGCTGCTGCTCCACGCGCGG 545
QY 536 AGCCCAACTGGCAGACCTGCCACTCTCACCCGACCGGTGCATGCTGCCCGGAGG 595
Db 546 AGCCCAACTGGCAGACCTGCCACTCTCACCCGACCGGTGCATGCTGCCCGGAGG 605
QY 596 GCTTCTTGACACGCTGGTGTGCTGCACGCGCGCGCGGTGGACGTGCGCGATG 655
Db 606 GCTTCTTGACACGCTGGTGTGCTGCACGCGCGCGCGGTGGACGTGCGCGATG 665
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Db 726 ACTTGGCAGACCGCGCGGAGTGA 751

RESULT 10
US-08-848-251-15
; Sequence 15, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.

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APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/848,251
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCI/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 335..751
US-08-848-251-15

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QY	299	CGGGCGGTGCG	CTGTGGGGGTTCGGAAT	TGCGGAGGAGAAACAAGGGCATGCCCAGTG	358
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QY	716	ACCTGCGAC	AGCCACGGGGACTGA	741	
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Qy	1	GAGGACTCCGGAGC-GTCCGACACCTCGGCCAGAGCGCTTTAGCTCGCTGCTTCC	59						
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Db	69	CGCTAGCGCTTTTCCAGAGCAATCCAGGCGCGCCGCTCGTTTGTAGAGCGCCAGG	128						
Qy	120	AAAGCCCGGAGCTAACGACCCGCGCGTCCG-CACTGCACGGGGCCCCACAGCCGACAG	178						
Db	129	AAAGCCCGGAGCTAACGACCCGCGCGTCCGCGCTGACGGGGCCCCAAGCCGC---AG	185						
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Db	186	AAGGACGACGGAGGGTAATGAAGCTGAGCCAGGCTCTCTAGGAAGAGAGAGTGGGCC	245						
Qy	239	GGACAGCGTGGGAAAGAGGGAAGTGTCTGTTAAGTTACGGCCAAACGGTGATTATC	298						
Db	246	GGACAGCGTGGGAAAGAGGGAAGTGTCTGTTAAGTTACGGCCAAACGGTGATTATC	305						
Qy	299	CGGCGCGTCCGCTGTGGGGCTGCGGAATGCGAGGAGAAACAGGGCATGCCAGTG	358						
Db	306	CGGCGCGTCCGCTGTGGGGCTGCGGAATGCGAGGAGAAACAGGGCATGCCAGTG	365						
Qy	359	GGGCGCGCAGCGATGAGGCTGTGCCA---CGCCGGCGGGGACTAGTGAGAGAGTGC	415						
Db	366	GGGCGCGCAGCGATGAGGCTGTGCCAGCGCCGCGCGCGGGGACTAGTGAGAGAGTGC	425						
Qy	416	GACACTCCTGGGAGCGGCGCGGATCCACAGGAGTCAACCGTTTCGGGAGGCGCGCGA	475						
Db	426	GACAGCTCCTGGAGCGGCGCGGATCCACAGGAGTCAACCGTTTCGGGAGGCGCGCGA	485						
Qy	476	TCCAGGTCATGATGGGACGCGCCGCTGCGGAGCTGCTGCTGCTCCACGGCGCGG	535						
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Qy	536	AGCCCACTGCGCAGACCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGAGG	595						
Db	546	AGCCCACTGCGCAGACCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGAGG	605						
Qy	596	GCTTCCTGGACACGCTGGTGTGTGCACCGGGCGCGGCTGGAGCTGGCGCATG	655						
Db	606	GCTTCCTGGACACGCTGGTGTGTGCACCGGGCGCGGCTGGAGCTGGCGCATG	665						
Qy	656	CCTGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGCCACCGGACCTTTCAGGGT	715						
Db	666	CCTGGGTCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGCCACCGGACCTTTCAGGGT	725						
Qy	716	ACCTGGCGACAGCCACGGGGGACTGA	741						
Db	726	ACCTGGCGACAGCCACGGGGGACTGA	751						

RESULT 14	
US-08-474-177-5	
Sequence 5, Application US/08474177	
Patent No. 5624819	
GENERAL INFORMATION:	
APPLICANT: Skolnick, Mark H.	
APPLICANT: Cannon-Albright, Lisa A.	
APPLICANT: Kamb, Alexander	
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE	
NUMBER OF SEQUENCES: 36	
CORRESPONDENCE ADDRESS:	
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP	
STREET: 1201 New York Avenue, Suite 1000	
CITY: Washington	
STATE: DC	
COUNTRY: USA	
ZIP: 20005	
COMPUTER READABLE FORM:	

Query Match	43.0%;	Score 360;	DB 1;	Length 1244;
Best Local Similarity	100.0%;	Pred. No. 1.7e-72;		
Matches 360;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	478	CAGGTCATGATGATGGCAGCGCCGCGTGGCGGAGCTGCTGCTCCACGGCGCGGAG	537
Db	271	CAGGTCATGATGATGGCAGCGCCGCGTGGCGGAGCTGCTGCTCCACGGCGCGGAG	330
QY	538	CCCAACTGGCAGACCTGCGACTCTACCCGACCGGTGCATGCTGCCGGGAGGCG	597
Db	331	CCCAACTGGCAGACCTGCGACTCTACCCGACCGGTGCATGCTGCCGGGAGGCG	390
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Db 451 TGGGGTCTGCTGCCGCTGGAGCTGGCCGAGGAGGGGGCCACCGCGAGCTTGAGGGTAC 510
Qy 718 CTGGCAGACAGCGGGGAGCTGACGCCAGGTTCCTCCAGCGCCGCCACACGACTTTATTT 777
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RESULT 15

US-08-487-033-5
; Sequence 5, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US/08/487,033
; APPLICATION NUMBER: RCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
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; NAME/KEY: intron

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US-08-487-033-5

Query Match 43.0%; Score 360; DB 2; Length 1244;
Best Local Similarity 100.0%; Pred. No. 1.7e-72;
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 538 CCCAACTGCGCAGACCCCTGCCACTCTCACCCGACCGGTGTCATGCTGCCCGGAGGC 597
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Qy 598 TTCTTGACACGCTGGT 657
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Qy 658 TGGGGTGTCTGCCCGTGGACTTTGGCCGAGGAGCGGGGCCACCGCGAGCTTGCAGGGTAC 717
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Db 511 CTGGCAGACAGCGGGGAGCTGACGCCAGGTTCCTCCAGCGCCGCCACACGACTTTATTT 570
Qy 778 TCTTACCAATTTCCCAACCCACCCACCTAATTCGATGAAGCTGCCACAGGGGAGCGG 837
Db 571 TCTTACCAATTTCCCAACCCACCCACCTAATTCGATGAAGCTGCCACAGGGGAGCGG 630

Search completed: July 21, 2000, 06:06:34
Job time: 13800 sec


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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:      July 21, 2000, 02:48:40 ; Search time 1049.06 Seconds
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Title:      US-09-016-869A-3
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Scoring table:  IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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2:  em_est2:*
3:  em_est3:*
4:  em_est4:*
5:  em_est5:*
6:  em_est6:*
7:  em_est7:*
8:  em_est8:*
9:  em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
31: gb_est12:*
32: gb_est13:*
33: gb_est14:*
34: gb_est15:*
35: gb_est16:*
36: gb_est17:*
37: gb_est18:*
38: gb_est19:*
39: gb_est20:*
40: gb_est21:*
41: gb_est22:*
42: gb_est23:*
43: gb_est24:*
44: gb_est25:*
45: gb_est26:*
46: gb_est27:*
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48: gb_est29:*
49: gb_est30:*
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52: em_est20:*
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55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_est45:*
80: gb_est46:*
81: gb_est47:*
82: em_est35:*
83: em_est36:*
84: em_est37:*
85: gb_est48:*
86: gb_est49:*
87: gb_est50:*
88: gb_est51:*
89: gb_est52:*
90: gb_est53:*
91: gb_est54:*
92: gb_est55:*
93: gb_gss1:*
94: gb_gss2:*
95: gb_gss3:*
96: gb_gss4:*
97: em_gss1:*
98: em_gss2:*
99: em_gss3:*
100: em_gss4:*
101: gb_gss5:*
102: gb_gss6:*
103: gb_gss7:*
104: gb_gss8:*
105: gb_gss9:*
106: em_gss5:*
107: em_gss6:*
108: em_gss7:*
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110: em_gss9:*
111: em_gss10:*
112: em_gss11:*
113: gb_gss10:*
114: gb_gss11:*
115: em_gss12:*
116: gb_gss12:*
```

```
117: gb_gss13: *
118: gb_gss14: *
119: gb_gss15: *
120: gb_gss16: *
121: gb_gss17: *
122: gb_gss18: *
123: gb_gss19: *
124: em_gss13: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
C	1	236.4	28.2	566	39	AI394605	AI394605 tg13g05.x
C	2	232	27.7	648	71	AW328496	AW328496 ds02h12.x
C	3	230	27.5	590	45	AI871381	AI871381 wl81d11.x
C	4	226.8	27.1	579	45	AI870879	AI870879 w177d11.x
C	5	225.2	26.9	580	38	AI362049	AI362049 qy39f07.x
C	6	224.2	26.8	579	36	AI198233	AI198233 q155d12.x
C	7	223.8	26.7	774	44	AI765096	AI765096 wk48b08.x
C	8	219.4	26.2	729	44	AI817709	AI817709 wk25c11.x
C	9	219.2	26.2	614	103	AQ496105	AQ496105 HS_5075_7
C	10	218.2	26.1	708	38	AI363262	AI363262 qy36f03.x
C	11	213.4	25.5	563	46	AI954684	AI954684 wq34h12.x
C	12	205.6	24.6	531	42	AI633790	AI633790 tl28e10.x
C	13	205.2	24.5	528	45	AI885362	AI885362 w192h04.x
C	14	204.6	24.4	528	42	AI638416	AI638416 tt31g03.x
C	15	203.8	24.3	579	62	AQ006218	AQ006218 wz39g05.x
C	16	201	24.0	480	79	AW631047	AW631047 hh91d11.y
C	17	194.8	23.3	526	31	AA089532	AA089532 zn44e11.r
C	18	191.8	22.9	526	32	AA909181	AA909181 o112b04.s
C	19	182.6	21.8	300	24	AA314567	AA314567 EST186468
C	20	181.6	21.7	599	28	AA557137	AA557137 nl74b05.s
C	21	173.8	20.8	516	47	AI989792	AI989792 wz27c06.x
C	22	167.8	20.0	531	44	AI806771	AI806771 wf15a09.x
C	23	158	18.9	505	36	AI186333	AI186333 qd30a08.x
C	24	157.8	18.9	496	71	AW328497	AW328497 ds02h12.y
C	25	154.6	18.5	548	32	AA903110	AA903110 ok52b03.s
C	26	149.6	17.9	533	32	AA877595	AA877595 nr07f06.s
C	27	147.8	17.7	494	69	AI90459	AI90459 xl15e01.x
C	28	142.8	17.1	531	33	AA946565	AA946565 oq49e06.s
C	29	131.6	15.7	563	45	AI869175	AI869175 wl150c04.x
C	30	129.2	15.4	450	35	AI091727	AI091727 ow59g04.x
C	31	117.4	14.0	689	38	AI337358	AI337358 tb98f09.x
C	32	113.4	13.5	465	44	AI818660	AI818660 wk89c11.x
C	33	109.2	13.0	441	20	AA055664	AA055664 zl75f06.s
C	34	103.6	12.4	588	40	AI499733	AI499733 tm91g12.x
C	35	103.2	12.3	606	44	AI798040	AI798040 wh80g12.x
C	36	102.6	12.3	533	64	AW169901	AW169901 xj34d12.x
C	37	101.6	12.1	419	46	AI937552	AI937552 w78f11.x
C	38	101.4	12.1	510	39	AI401012	AI401012 t99f104.x
C	39	101.2	12.1	421	40	AI749957	AI749957 tm73d10.x
C	40	100.6	12.0	550	37	AI245973	AI245973 qk45d10.x
C	41	99.8	11.9	539	63	AQ055075	AQ055075 wy99c10.x
C	42	99.6	11.9	557	42	AI566826	AI566826 tt54c09.x
C	43	99.4	11.9	537	36	AI221498	AI221498 qg87a12.x
C	44	99.4	11.9	597	43	AI703354	AI703354 wd93c07.x
C	45	99.2	11.9	522	34	AI057178	AI057178 oy78b02.x

ALIGNMENTS

RESULT	1
AI394605/C	
LOCUS	AI394605 566 bp mRNA EST 30-MAR-1999
DEFINITION	tg13g05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR

Query Match 26.9%; Score 225.2; DB 38; Length 580;
Best Local Similarity 91.2%; Pred. No. 3.3e-42;
Matches 239; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 477 CCAGGTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGGA 536
DB 557 CCAGGTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGGA 498
QY 537 GCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGG 596
DB 497 GCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGG 438
QY 597 CTTCTGGACACGCTGGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGC 656
DB 437 CTTCTGGAACACGCTGGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGC 378
QY 657 CTGGGTCGTCCTCCGCTGGACTTGGCCGAGGAGCGGGCCACCGACGTTTCAGGGTA 716
DB 377 CTGGGTCGTCCTCCGCTGGACTTGGCCGAGGAGCTGGGCGCATGCGGATGTCGACGGTA 318
QY 717 CTTGCGACAGCCACGGGGGAC 738
DB 317 CTTGCGCGGCTGCGGGGGGCG 296

RESULT 6
AI198233/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI198233 579 bp mRNA EST 02-DEC-1998
g155d12 x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.B3 TARI TARI repetitive element ;, mRNA sequence.

AI198233
AI198233.1 GI:3750839
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BrGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 729 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
1. .579
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1860407"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"

FEATURES
source

QY 478 CAGGTTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGAG 537
DB 555 CAGGTTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGAG 496
QY 538 CCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGGC 597
DB 495 CCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGGC 436
QY 598 TTCTCTGGACACGCTGGTGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657
DB 435 TTCTCTGGACACGCTGGTGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 376
QY 658 TGGGTCGCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGCGGCTGGACGTGCGCGATGCC 717
DB 375 TGGGTCGCTGCTGCCCGTGGACTTGGCCGAGGAGCTGGGCGCATGCGGACGTTAC 316
QY 718 CTGCGCACAGCCACGGGGGAC 738
DB 315 CTGCGCGGCTGCGGGGGGCG 295

RESULT 7
AI765096/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI765096 774 bp mRNA EST 21-DEC-1999
wi48b08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393433 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.B3 MER22 repetitive element ;, mRNA sequence.

AI765096
AI765096.1 GI:5231605
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
Location/Qualifiers
1. .774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col6"

FEATURES
source

T 3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 158 c 177 g 130 t 1 others.
ORIGIN

Query Match 26.8%; Score 224.2; DB 36; Length 579;
Best Local Similarity 91.2%; Pred. No. 5.6e-42;
Matches 238; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 478 CAGGTTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGAG 537
DB 555 CAGGTTCATGATGGGAGCGCCGCTGGCGGAGCTGCTGCTCCACGGCGGAG 496
QY 538 CCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGGC 597
DB 495 CCCAACTGGCGAGACCTGCCACTCTCACCCAGCGGTGCATGCTGCCCGGGAGGGC 436
QY 598 TTCTCTGGACACGCTGGTGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 657
DB 435 TTCTCTGGACACGCTGGTGTGTGTGCACCGGGCGGGCGGCTGGACGTGCGCGATGCC 376
QY 658 TGGGTCGCTGCTGCCCGTGGACTTGGCCGAGGAGCGGGCGGCTGGACGTGCGCGATGCC 717
DB 375 TGGGTCGCTGCTGCCCGTGGACTTGGCCGAGGAGCTGGGCGCATGCGGACGTTAC 316
QY 718 CTGCGCACAGCCACGGGGGAC 738
DB 315 CTGCGCGGCTGCGGGGGGCG 295

RESULT 7
AI765096/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI765096 774 bp mRNA EST 21-DEC-1999
wi48b08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393433 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.B3 MER22 repetitive element ;, mRNA sequence.

AI765096
AI765096.1 GI:5231605
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
Location/Qualifiers
1. .774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col6"

FEATURES
source


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QY 622 CACCGGCGGGCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTG 681
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 411 CACCGGCGGGCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTG 352
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 682 GCGGAGGAGGGGCGCACCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTG 738
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 351 GCTGAGGAGTGGGCGCATGCGCATGCTGGACGCTACTGCGCGCGGTGCGGGGGG 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
AI885362/c 528 bp mRNA EST 07-MAR-2000
LOCUS w192h04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3'
DEFINITION similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; mRNA sequence.
ACCESSION AI885362
VERSION AI885362.1 GI:5590526
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute / National Institute of Neurological
COMMENT Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCGAAGTGGGCGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 165 g 114 t
ORIGIN
Query Match 24.5%; Score 205.2; DB 45; Length 528;
Best Local Similarity 92.3%; Pred. No. 1.3e-37;
Matches 216; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 505 GTGCGGAGTGTGCTGCTCCACGGCGGAGCCCAACTGCGCAGACCTGCGCACTTC 564
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 528 GTGCGGAGTGTGCTGCTCCACGGCGGAGCCCAACTGCGCAGACCTGCGCACTTC 469
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 565 ACCGACCGGTGATGATGCTGCCCGGAGGGCTTCTCGACACGCTGTGCTGCTGCAC 624
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 468 ACCGACCGGTGATGATGCTGCCCGGAGGGCTTCTCGACACGCTGTGCTGCTGCAC 409
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 625 CCGGCGGGGCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTGCC 684
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 408 CCGGCGGGGCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTGCC 349
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 685 GAGGACGGGGCGCGCGGTGGACGTGCGCATGCTGGGGTGTGTCGCCCGTGACTTG 738
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 348 GAGGAGTGGGGCATGCGCATGCTGGACGCTACTGCGCGCGGTGCGGGGGG 295
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AI638416/c 528 bp mRNA EST 14-DEC-1999
LOCUS tt31g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
DEFINITION similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.b3 TAR1 repetitive element ; mRNA sequence.
ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
FEATURES
source
Location/Qualifiers
1..528
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI-CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 163 g 114 t
ORIGIN
Query Match 24.4%; Score 204.6; DB 42; Length 528;
Best Local Similarity 91.1%; Pred. No. 1.8e-37;
Matches 216; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy 622 CACCGGGCGGGCGGGCTGACGTGGCGGATGCTGGGGTCTGCTCCCGTGGACTTG 681
Db 408 CACCGGGCGGGCGGGCTGACGTGGCGGATGCTGGGGTCTGCTCCCGTGGACTTG 349
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RESULT 15
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DEFINITION w293905.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566424 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.

ACCESSION AW006218
VERSION AW006218.1 GI:5854996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
On Oct 6, 1998 this sequence version replaced gi:3705694.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco
High quality sequence stop: 461.
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1. 579
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/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCCATAGTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 113 a 161 c 172 g 131 t 2 others
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Matches 239; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

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Db 499 GGAGCCCAANTGGCGGAGCCG-GCCACTCTCACCCGACCGGTGCACGACGCTGCCCGGGA 441
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Search completed: July 21, 2000, 02:48:45
Job time: 9640 sec

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Date: Jul 21, 2000 8:05 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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Search information block:

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gb_pat:AR037506	+	667.50	6.9e-43	751	AR037506 Sequence 15 from patent
gb_pat:AR062786	+	667.50	6.9e-43	751	AR062786 Sequence 15 from patent
gb_pat:141160	+	667.50	6.9e-43	751	I41160 Sequence 15 from patent
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gb_ro:AF059567	+	550.00	9.2e-34	1301	AF059567 Mus musculus cyclin d
gb_pat:AR062815	+	545.50	7.1e-34	393	AR062815 Sequence 45 from patent
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gb_pat:AR037494	+	506.50	6.99.13	471	AR037494 Sequence 1 from patent
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DEFINITION	Homo sapiens (clone p15INK4B/HAS) CDK inhibitory protein mRNA,					
	complete cds.					
ACCESSION	L36844					
VERSION	L36844.1 GI:556197					
KEYWORDS	CDK inhibitory protein.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
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	Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 837)					
AUTHORS	Hannon,G.J. and Beach,D.					
TITLE	p15INK4B is a potential effector of TGF-beta induced cell cycle					
JOURNAL	Nature 371, 257-261 (1994)					
MEDLINE	94359613					
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51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH 67						
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728 CCACGGGGGAC 738
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LOCUS HSD17075 738 bp mRNA PRI 27-JAN-1995
DEFINITION Human p14-CDK inhibitor mRNA, complete cds.
ACCESSION U17075
VERSION U17075.1 GI:639715
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 738)
AUTHORS Guan,K.L., Jenkins,C.W., Li,Y., Nichols,M.A., Wu,X., O'Keefe,C.L.,
Matera,A.G. and Xiong,Y.
Growth suppression by p18, a p16INK4/MTS1- and
p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type prb
function
JOURNAL Genes Dev. 8 (24), 2939-2952 (1994)
MEDLINE 95095079
REFERENCE 2 (bases 1 to 738)
AUTHORS Guan,K.
TITLE Direct Submission
Submitted (09-NOV-1994) Kun-Liang Guan, Biological Chemistry,
University of Michigan, 1301 East Catherine, Ann Arbor, MI 48109,
USA
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ACCESSION AR001326
VERSION AR001326.1 GI:3963393
KEYWORDS
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ORGANISM Unclassified.
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AUTHORS Kamb,A.
TITLE MTS1E1.beta. gene
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DEFINITION Sequence 15 from patent US 5801236.
ACCESSION AR037506
VERSION AR037506.1 GI:5955362
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 751)
AUTHORS Kamb, A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 15 01-SEP-1998;
FEATURES
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REFERENCE 1 (bases 1 to 751)
AUTHORS Stone, S., Jiang, P. and Kamb, A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 15 01-DEC-1998;
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50  IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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485  ATCAGGTCTATGATGTGGCAGCGCCGCTGGCGAGCTGCTGCT 534
|||||
66  uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
|||||
```

```
|||||
535 CCACGGCGGAGCCCACTGCGCAGACCCTCCCACTCACCACCGG 584
83 aHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
|||||
585 TCATGATGCTGCCCGGGAGGCTTCTTGGACACGCTGGTGGTGCAC 634
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProva 116
|||||
635 CGGGCGGGCGCGCTGACGTGGCGATGCTGGGTCTGCTGCCGT 684
116 lasLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCCGAGGCGGGCCACCGCAGCTTGCAGGGTACCTGCCA 734
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGAC 748
seq_name: gb_pat:141160
seq_documentation_block:
LOCUS I41160 751 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 15 from patent US 5624819.
ACCESSION I41160
VERSION I41160.1 GI:2081750
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 751)
AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
TITLE Germ-line mutations in the MTS gene
JOURNAL Patent: US 5624819-A 15 29-APR-1997;
FEATURES
Location/Qualifiers
source
1..751
/organism="unknown"
BASE COUNT 130 a 225 c 292 g 104 t
ORIGIN
alignment_scores:
Quality: 667.50 Length: 138
Ratio: 4.981 Gaps: 1
Percent Similarity: 97.101 Percent Identity: 95.652
alignment_block:
US-09-016-869a-4 x I41160 ..
Align seg 1/1 to: I41160 from: 1 to: 751
1 MetArgGluAsnLysGlyMetProSerGlyGlySerAspGluG 17
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335 ATGCGGAGGAGAACAAAGGCGATGCCAGTGGGCGGCAGCGATGAGG 384
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
385 TCTGGCACCGCGCGCGCGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgGAla 49
|||||
435 TGGACCGCGCGGATCCACAGGAGTCAACCGTTTCGGGAGGCGCGG 484
50 ileGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
|||||
485 ATCCAGGTATGATGATGGCAGCGCGCGTGGGAGCTCTGCTGCT 534
66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
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535 CCACGCGCGGAGCCCACTGCGCAGACCCTGCCACTCTCACCCACCGG 584
83 aHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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585 TGCATGATGCTGCCCGGGAGGCTTCTTGGACACGCTGGTGGTGCAC 634
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProva 116
|||||
635 CGGGCGGGCGCGCTGACGTGGCGATGCTGGGTCTGCTGCCGT 684
116 lasLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCCGAGGCGGGCCACCGCAGCTTGCAGGGTACCTGCCA 734
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGAC 748
seq_name: gb_pr3:AF004819
seq_documentation_block:
LOCUS AF004819 859 bp mRNA PRI 11-SEP-1997
DEFINITION Homo sapiens alternative spliced form of p15 CDK inhibitor mRNA,
complete cds.
ACCESSION AF004819
VERSION AF004819.1 GI:2257934
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 859)
AUTHORS Tsubari,M., Tiihonen,E. and Laiho,M.
TITLE Cloning and characterization of p10, an alternatively spliced form
of p15 cyclin-dependent kinase inhibitor
JOURNAL Cancer Res. 57 (14), 2966-2973 (1997)
MEDLINE 97373727
REFERENCE
2 (bases 1 to 859)
AUTHORS Tsubari,M., Tiihonen,E. and Laiho,M.
TITLE Direct Submission
JOURNAL Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
University of Helsinki, P.O. Box 21, Helsinki 00014, Finland
FEATURES
Location/Qualifiers
source
1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
320..556
/contig="p10"
/codon_start=1
/product="alternative spliced form of p15 CDK inhibitor"
/protein_id="AAB69989.1"
/db_xref="GI:2257935"
/translation="MREENKMGPSGGSGDEGLASAAARGLVEKVRQLLEAGADPNGVN
RFERRAIQVAGAPGPRRQRRERGARPRRIGAGT"
BASE COUNT 144 a 257 c 338 g 120 t
ORIGIN
alignment_scores:
Quality: 637.00 Length: 179
Ratio: 4.754 Gaps: 2
Percent Similarity: 74.860 Percent Identity: 73.743
alignment_block:
US-09-016-869a-4 x AF004819 ..
Align seg 1/1 to: AF004819 from: 1 to: 859
1 MetArgGluAsnLysGlyMetProSerGlyGlySerAspGluG 17
|||||
320 ATGCGGAGGAGAACAGGCGATGCCAGTGGGCGGCAGCGATGAGG 369
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
|||||
370 TCTGGCCAGCGCGCGGGGACTAGTGGAGAAGGTGCGACAGCTCC 419
33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgGAla 49
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420 TGGAGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGAGGCGCGC 469

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50 Ilegln..... 51

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470 ATCCAGGTAGCTGGGGCCCGCAGGGCTCGCGGAGGGGCGCGGAACG 519

|||||
51 51

520 CGGCGCGCGCTCGGCGGATCGGGGCTGGAACCTAGATCGCGGATGAG 569

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52ValMetMetMetGlySerAla 58

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570 ATTGTACAGAGTCTCGTTGGCGGAGGTCATGATGGGAGCGGCC 619

|||||
59 ArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAs 75

|||||
620 CGCGTGGCGAGCTGCTGCTCCACGCGGAGGCCCACTGCGCAGA 669

|||||
75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92

|||||
670 CCCTGCCACTCTCACCGACCGGTGCATGATGCTGCCGCGGAGGCTTCC 719

|||||
92 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 108

|||||
720 TGGACAGCTGCTGCTGCTCACCGCGCGGCGGCTGAGCTGCGC 769

|||||
109 AspAlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisAr 125

|||||
770 GATGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819

|||||
125 gAspValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137

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820 CGAGCTTGCAGGGTACCTGCGCACGACGCGGGGAC 856

seq_name: gb_ro:S79760

seq_documentation_block: 706 bp mRNA ROD 02-FEB-1996

LOCUS S79760
DEFINITION Ink4 [rats, kidney, mRNA, 706 nt].
ACCESSION S79760

VERSION S79760.1 GI:1176432
KEYWORDS Rattus sp. kidney.

SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 706)
AUTHORS Hino, O., Kobayashi, E., Hirayama, Y., Kobayashi, T., Kubo, Y.,
Tsuchiya, H., Kikuchi, Y. and Mitani, H.

TITLE Molecular genetic basis of renal carcinogenesis in the Eker rat
model of tuberosus sclerosis (TSC2)

JOURNAL Mol. Carcinog. 14 (1), 23-27 (1995)
MEDLINE 96001392

REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 171930] from the original journal article.

Map location: 5q.
Location/Qualifiers

1. .706
/organism="Rattus sp."
/db_xref="taxon:10118"

161. .553
/gene="Ink4"

161. .553
/gene="Ink4"

/note="This sequence comes from Fig. 1A"

/codon_start=1
/protein_id="AAB35360.1"

/db_xref="GI:1176432"

/translation="MLGGSDAGLATAAARGOVETVROLLEAGADPNVNRFRRIQ
VMMGSAOVAEILLHLHGAEPNCADPATLTPVHDAAREGFLDTLVHLKAGARLDVCD
ANGRPVDAEEQGHDIARYLHAATGD"

BASE COUNT 142 a 212 c 231 g 121 t
ORIGIN

alignment_scores:
Quality: 555.00 Length: 137
Ratio: 4.512 Gaps: 2

Percent Similarity: 89.781 Percent Identity: 82.482

alignment_block:

US-09-016-869A-4 x S79760 ..

Align seg 1/1 to: S79760 from: 1 to: 706

2 ArgGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLe 18
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143 CGGACCGGGGACAAAGGCATG...TTGGGGCGGCGAGTGACGGGGCT 189

18 uAlaThr....ProAlaArgGlyLeuValGluLysValArgHisSerTrpG 34
|||||
190 GCCCACCAGCGCGCGGGGACAGGTGGAGACGGTGGCAGCTCCTGG 239

34 luAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAlaAla 50
|||||
240 AAGCGGCGCAGATCCCAACGCCGTCAACCGCTTCGGGAGCGGCCGATC 289

51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuH 67
|||||
290 CAGGTATGATGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 339

67 sGlyValAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||
340 CGGAGCAGAACCCCACTGCCCGGATCTGCCACCTCACCAGACCTGTGC 389

84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
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390 ATGATGAGCTCGAGAGGGCTTCTGGACAGCTAATGGTGTGCACAAG 439

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||
440 GCAGGGCAGCGCTGGATGTGTGTGACGCTGGGCGGCGGCGGCGGCGG 489

117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
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490 CTTAGCTGAAGAGCAGGGCCACCGTGTATTTGCGAGGTATCTGCACGCTG 539

134 laThrGlyAsp 137
|||||

540 CCACCTGGAGAT 550

seq_name: gb_ro:AF059567

seq_documentation_block: 1301 bp mRNA ROD 22-APR-1998

LOCUS AF059567
DEFINITION Mus musculus cyclin dependent kinase inhibitor 2B (Cdkn2b) mRNA,
complete cds.

ACCESSION AF059567
VERSION AF059567.1 GI:3075496

KEYWORDS house mouse.
SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1301)
AUTHORS Quelle, D.E., Ashmun, R.A., Hannon, G. J., Rehberger, P. A., Trono, D.,
Richter, K. H., Walker, C., Beach, D., Sherr, C. J. and Serrano, M.

TITLE Cloning and characterization of murine p16INK4a and p15INK4b genes
JOURNAL Oncogene 11 (4), 635-645 (1995)

MEDLINE 95380169
REFERENCE 2 (bases 1 to 1301)

AUTHORS Quelle, D.E., Ashmun, R.A., Hannon, G. J., Rehberger, P. A., Trono, D.,
Richter, K. H., Walker, C., Beach, D., Sherr, C. J. and Serrano, M.

TITLE Direct Submission

JOURNAL Submitted (14-APR-1998) Immunology and Oncology, National Center of
Biotechnology, Campus de Cantoblanco, Madrid E-28049, Spain

FEATURES

source
1. .1301
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/map="C3-C6"
/cell_line="p19"
/cell_type="embryonal carcinoma"
1. .1301
/gene="Cdkn2b"
145. .537
/gene="Cdkn2b"
/function="inhibitor of CDK4 and CDK6"
/note="p15INK4b; CDKN2B"
/codon_start=1
/product="cyclin dependent kinase inhibitor 2B"
/protein_id="AAC14569.1"
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/translation="MLGSSDAGLATAAARGQVETVROLLEAGADPNALNRFGRRTIQ
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BASE COUNT 322 a 347 c 361 g 271 t
ORIGIN

alignment_scores:
Quality: 550.00 Length: 134
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Percent Similarity: 91.045 Percent Identity: 83.582

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136 GACAAGGGCATG...TTGGCGCGGACAGTGCAGCGGCGCTGGCCACCGC 182
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
183 CGCGGCGCGGGGCAAGTGGAGACGGTGGCGAGCTCTGGAGCGGGG 232
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
233 CAGATCCCAACGCCCTGAACCGCTTCGGGAGGCGCCCAATCCAGGTCTATG 282
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyValAcl 70
283 ATGATGGGCGAGCGCCGAGTGGCAGAGTGTCTGCTCCACGAGCAGA 332
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
333 ACCCAACTCGCGGACCCCTGCCACCTTACCAGACCTGTGTGACGACGAC 382
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
383 CTCGGGAGAGCTTCTGGACAGCTGTCTGCTGCACCGGCGGGGGG 432
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaCl 120
433 CGGCTGGATGTGTGACCGCTGGGCGCCCTGGCGGTAGACTGGCTGA 482
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137
483 AGAGCAGGCGCCACCGTGACATGCCAGGTATCTGCACGCTGCCACTGGAG 532
137 sp 137
533 AT 534

seq_name: gb_pat:AR062815

seq_documentation_block:

LOCUS AR062815 393 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5843756.
ACCESSION AR062815
VERSION AR062815.1 GI:5990506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 393)
AUTHORS Stone, S., Jiang, P. and Kamb, A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 45 01-DEC-1998;
FEATURES Location/Qualifiers
1. .393
source
BASE COUNT 69 a 124 c 141 g 59 t
ORIGIN

alignment_scores:
Quality: 545.50 Length: 128
Ratio: 4.623 Gaps: 1
Percent Similarity: 92.188 Percent Identity: 85.156

alignment_block:

US-09-016-869a-4 x AR062815 ..

Align seg 1/1 to: AR062815 from: 1 to: 393

11 GlyGlyGlySerAspGluGlyLeuAlaThr...ProAlaArgGlyLeuVa 26
7 GCGGCGACAGTGCAGCGGCGCTGGCCACCGCGCGCGGGGCAAGT 56
26 lclLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyValA 43
57 GGAGACGGTGGCGCAACTCTGTGAAGCGCGGCGAGATCCCAACGCCCTGA 106
43 snArgPheGlyArgAlaIleGlnValMetMetMetGlySerAlaArg 59
107 ACCGCTTCGGGAGGCGCCCAATCCAGGTTCATGATGGCGAGCGCCAG 156
60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76
157 GTGGCAGAGCTGTCTGCTCCACGAGCAGAACCCAACTGCGCGGACCC 206
76 oAlaThrLeuThrArgProValHisAspAlaArgGluGlyPheLeuA 93
207 TGCCACCTTACCAGACCTGTGCAGCGAGCTCGGAAGGCTTCCTGG 256
93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
257 ACACGCTTGTGCTGTCGACCGCGGCGCGGCTGATGTGTGTGAC 306
110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126
307 GCCTGGGCGCGCTGCCGCTAGACTTGGCTGAAGAGCAGGAGCCACCGTGA 356
126 pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
357 CATTCGAGAGGTATCTGCACGCTGCCACTGGAGAT 390
seq_name: gb_pat:AR001314

seq_documentation_block:
LOCUS AR001314 471 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5739027.
ACCESSION AR001314
VERSION AR001314.1 GI:3963381
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kamb,A.
TITLE MTS1 beta, gene
JOURNAL Patent: US 5739027-A 1 14-APR-1998;
FEATURES
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BASE COUNT 68 a 153 c 186 g 64 t
ORIGIN

alignment_scores:
    Quality: 506.50 Length: 133
    Ratio: 4.404 Gaps: 2
    Percent Similarity: 86.466 Percent Identity: 80.451
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US-09-016-869A-4 x AR001314 ..
Align seg 1/1 to: AR001314 from: 1 to: 471
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7 CCGCGCGGGGAGCAGCATGCGGCTTCGGCTGACTGGCTGGCCACGCG 56
|||||:|||||:|||||:|||||:
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||:|||||:|||||:|||||:
57 CCGCGCGGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGGG 106
|||||:|||||:|||||:|||||:
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
|||||:|||||:|||||:|||||:
107 CGCTGCCACCGCCGAAATAGTTACGGTCGGAGCCCATCCAGGTCTATG 156
|||||:|||||:|||||:|||||:
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
|||||:|||||:|||||:|||||:
157 ATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTGCCACGCGCGGA 206
|||||:|||||:|||||:|||||:
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
|||||:|||||:|||||:|||||:
207 GCCCAACTGCCCGCCGAGTGGCGGAGCTGCTGCCACGCGCGCGA 256
|||||:|||||:|||||:|||||:
87 laArgGluGlyPheLeuAspThrLeuValAlaLeuHisArgAlaGlyAla 103
|||||:|||||:|||||:|||||:
257 CCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTGCACCGCGCGGGCG 306
|||||:|||||:|||||:|||||:
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
|||||:|||||:|||||:|||||:
307 CGGCTGGACGTCCGCGATGCTGGCGCGCTGCTGCCGTGGACCTGGCTGA 356
|||||:|||||:|||||:|||||:
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||:|||||:|||||:|||||:
357 GGAGCTGGGCCATCGCATGTCGACGCTACCTGCGCGCGCTGCGGGG 405
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seq_name: gb_pat:AR062774

seq_documentation_block:
LOCUS AR062774 471 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5843756.
ACCESSION AR062774
VERSION AR062774.1 GI:5990465
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Stone,S., Jiang,P. and Kamb,A.
TITLE Mouse MTS1 gene
JOURNAL Patent: US 5843756-A 1 01-DEC-1998;
FEATURES
    source 1..471
    /organism="unknown"
BASE COUNT 68 a 153 c 186 g 64 t
ORIGIN

alignment_scores:
    Quality: 506.50 Length: 133
    Ratio: 4.404 Gaps: 2
    Percent Similarity: 86.466 Percent Identity: 80.451
alignment_block:
US-09-016-869A-4 x AR037494 ..
Align seg 1/1 to: AR037494 from: 1 to: 471
9 ProSerGlyGlySerAspGlu.....GlyLeuAlaThr.. 20
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7 CCGCGCGGGGAGCAGCATGCGGCTTCGGCTGACTGGCTGGCCACGCG 56
|||||:|||||:|||||:|||||:
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||:|||||:|||||:|||||:
57 CCGCGCGGGGTCGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGGG 106
|||||:|||||:|||||:|||||:
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
|||||:|||||:|||||:|||||:
107 CGCTGCCACCGCCGAAATAGTTACGGTCGGAGCCCATCCAGGTCTATG 156
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54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
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157 ATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCCACGCGCGGA 206
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70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
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207 GCCCAACTGCCCGCCGAGTGGCGGAGCTGCTGCCACGCGCGCGA 256
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87 laArgGluGlyPheLeuAspThrLeuValAlaLeuHisArgAlaGlyAla 103
|||||:|||||:|||||:|||||:
257 CCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTGCACCGCGCGGGCG 306
|||||:|||||:|||||:|||||:
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
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307 CGGCTGGACGTCCGCGATGCTGGCGCGCTGCTGCCGTGGACCTGGCTGA 356
|||||:|||||:|||||:|||||:
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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357 GGAGCTGGGCCATCGCATGTCGACGCTACCTGCGCGCGCTGCGGGG 405
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seq_name: gb_pat:AR037494

seq_documentation_block:
LOCUS AR037494 471 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5801236.
ACCESSION AR037494
VERSION AR037494.1 GI:5955350
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 471)
AUTHORS Kamb,A.
TITLE Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL Patent: US 5801236-A 1 01-SEP-1998;
FEATURES
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alignment_block:

US-09-016-869A-4 x AR062774

Align seg 1/1 to: AR062774 from: 1 to: 471

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7 CCGCGCGCGGGGAGCAGCATGGAGCCCTTCGGCTGACTGGCTGCCACGGC 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 CCGCGCGCGGGGTCGGGTAGAGAGGTGCGGCGCTGCTGGAGCGGGG 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 laaspProasnGlyValasnArgPheGlyArgAlaIleGlnValMet 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 CGTGGCCCAACGCCAGCAATAGTTACGGTGGAGCGCATCCAGGTCATG 156
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54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 ATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGGCGCGGA 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 laaspProasnGlyValasnArgPheGlyArgAlaIleGlnValMet 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 CGTGGCCCAACGCCAGCAATAGTTACGGTGGAGCGCATCCAGGTCATG 156
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54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
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157 ATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCACGGCGCGGA 206
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70 uProasnCysAlaaspProAlaThrLeuThrArgProValHisAspAlaA 87
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207 GCCCAACTGCGCGACCCGCCACTCTCACCCGACCGCTGCACGACGCTG 256
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LOCUS I41148 471 bp DNA PAT 13-MAY-1997

DEFINITION Sequence 1 from patent US'5624819.

ACCESSION I41148

VERSION I41148.1 GI:2081738

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 471)

AUTHORS Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.

TITLE Germline mutations in the MTS gene

JOURNAL Patent: US 5624819-A 1 29-APR-1997;

FEATURES

Location/Qualifiers

1..471

/organism="unknown"

BASE COUNT 68 a 153 c 186 g 64 t

ORIGIN

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Quality: 506.50 Length: 133
Ratio: 4.404 Gaps: 2
Percent Similarity: 86.466 Percent Identity: 80.451

alignment_block:

US-09-016-869A-4 x I41148

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LOCUS AR001346 947 bp DNA PAT 04-DEC-1998

DEFINITION Sequence 36 from patent US 5739027.

ACCESSION AR001346

VERSION AR001346.1 GI:3963413

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 947)

AUTHORS Kamb,A.

TITLE MTS1E1.beta. gene

JOURNAL Patent: US 5739027-A 36 14-APR-1998;

FEATURES

Location/Qualifiers

1..947

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ORIGIN

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US-09-016-869A-4 x AR001346

Align seg 1/1 to: AR001346 from: 1 to: 947

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21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
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257 CCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGCGCGGGGCG 306
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGl 120
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307 CGGCTGGACGTGCCGATGCTTGGGGCCGCTGCCCTGGACCTGGGCTGA 356
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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357 GGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGCTCGGGGG 405
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about. Results were produced by the GenCore
Copyright (c) 1993-2000 Compugen Ltd.

Search information block:

Query length: 137

Database sequences: 311585

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N_Genesed_36:T69781	+	667.50	1163.10	3.5e-57	751	Human multiple tumour suppress
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N_Genesed_36:T26232	+	513.00	889.13	6.3e-42	1073	Truncated p27/p16 fusion prote
N_Genesed_36:T26234	+	509.00	884.92	1.1e-41	782	Truncated p27/p16 fusion prote
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N_Genesed_36:T53819	+	506.50	885.02	1.1e-41	471	Nucleotide sequence of the CDS
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N_Genesed_36:Q99158	+	493.50	862.70	1.9e-40	447	Human multiple tumour suppress
N_Genesed_36:Q63491	+	493.50	856.04	4.4e-40	948	Inhibitor of cyclin dependent
N_Genesed_36:T00749	+	486.50	850.43	1.9e-40	447	Multiple tumour suppressor 1 (M
N_Genesed_36:T00750	+	485.50	848.67	1.4e-39	447	Multiple tumour suppressor 1 (M
N_Genesed_36:T00741	+	451.00	779.14	8.5e-36	1244	Multiple tumour suppressor 2 (
N_Genesed_36:Q99168	+	451.00	779.14	8.5e-36	1244	Human MTS2 DNA including exon
N_Genesed_36:V11241	+	451.00	779.14	8.5e-36	1244	Human MTS2 genomic DNA includ
N_Genesed_36:V53822	+	451.00	779.14	8.5e-36	1244	Nucleotide sequence of the mul

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 585 TGCATGATCTCCCGGGAGGCTCTCTGGACACGCTGGTGTGTGCAC 634
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 AC Q99165;
 DT 03-MAY-1996 (first entry)
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 KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
 KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
 KW gene therapy; chronic; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 335..751
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 PD W09525429-A1.
 PN 28-SEP-1995.
 PR 17-MAR-1995; U03316.
 PR 18-MAR-1994; US-214581.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 95-344401/44.
 DR P-PSDB; R80948.
 PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.,
 PT melanoma or leukaemia
 PS Claim 3; Page 102-103; 156pp; English.
 CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
 CC polypeptides have been isolated and sequenced. This sequence encodes
 CC the MTS polypeptide MTS2 (R80948). MTS polypeptide-encoding cDNAs
 CC and mutants of these are useful for the diagnosis or prognosis of
 CC human cancer. Germ-line mutations of MTS cDNAs can be used for
 CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,
 CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers
 CC of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and
 CC rectum. The wild-type gene is useful for gene therapy and MTS
 CC polypeptides may also be used for protein replacement therapy. Also
 CC screening for potential cancer therapeutics.
 SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

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 Percent Similarity: 97.101 Percent Identity: 95.652

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 AC T69781;
 DT 10-SEP-1997 (first entry)
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 KW Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT cds 335..751
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 PN 29-APR-1997.
 PD 18-MAR-1994; 214582.
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 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03537.
 PR 07-JUN-1995; US-474177.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI; 97-258217/23.
 DR P-PSDB; W19255.
 PT Human mutant multiple tumour suppressor gene sequences - for
 PT production of recombinant mutant polypeptide(s)
 PS Disclosure; Columns 75-78; 72pp; English.
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635 CGGCGCGGGCGCGCTGGACGTGCGCGATGCCCTGGGGTCTGCTGCCG 684

116 lAspLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
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  KW germ-line mutation; familial melanoma locus; MLM; Predisposition; ds.
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  FT /note= "multiple tumour suppressor"
  PN US5739027-A.
  PD 14-APR-1998.
  PR 07-JUN-1995; 487033.
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  PR 18-MAR-1994; US-214582.
  PR 18-MAR-1994; US-215086.
  PR 18-MAR-1994; US-215087.
  PR 14-APR-1994; US-227369.
  PR 01-JUN-1994; US-251938.
  PR 17-MAR-1995; WO-U03316.
  PA (MYRI-) MYRIAD GENETICS INC.
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PI Kamb A;
DR WPI; 98-250421/22.
DR P-PSDB; W40526.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PS Disclosure; Fig 11; 72pp; English.
CC This cDNA sequence encodes a human multiple tumour suppression protein,
CC MTS2. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
  Quality: 667.50      Length: 138
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  Percent Similarity: 97.101  Percent Identity: 95.652

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385 TCTGCCACAGCCCGCGCGGGGAGCTAGTGGAGAGGTGGCAGACTCC 434

33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
|||||
435 TGGAGCGCGCGCGGATGCCAACGAGTCAACCGTTTCGGGAGGCGCG 484

50 lIeGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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485 ATCCAGGTGATGATGGGCGAGCGCGCGTGGCGGAGTCTGCTGCT 534

56 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProv 83
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  DT 04-DEC-1998 (first entry)
  DE Coding sequence 2 of the multiple tumour suppressor MTS1E1S.
  DE Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
  KW somatic mutation; gene therapy; ds.
  OS Homo sapiens.
```

```

FH Key          Location/Qualifiers
FT CDS          335..751
FT FT           /*tag= a
FT FT           /product= "human MTS1E1s"
PD US5801236-A.
PD 01-SEP-1998.
PD 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PR (MYRI-) MYRIAD GENETICS INC.
PA Kamb A;
DR WPI: 98-494842/42.
DR P-PSDB; W74553.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure; Fig 11: 73pp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor
CC (MTS1E1s) gene, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic acid hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101 Percent Identity: 95.652

alignment_block:
  US-09-016-869A-4 x V53831  ..
  Align seg 1/1 to: V53831 from: 1 to: 751

  1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
    |||||
  335 ATGCGCGAGGAGAACAAAGGGCATGCCAGTGGGGCGGCAGCGATGAGG 384
    |||||
  17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
    |||||
  385 TCTGGCCAGCCCGCGCGGGGACATAGTGGAGAAAGTGGCAGCTCC 434
    |||||
  33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
    |||||
  435 TGGAAAGCGCGCGGATGCCAACAGGAGTCAACCGTTTCGGGAGCGCGG 484
    |||||
  50 IlegInValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
    |||||
  485 ATCCAGGTCTATGATGATGGGCGAGCGCGCGTGGCGAGCTGCTGCT 534
    |||||
  66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgPro 83
    |||||
  535 CCACGGCGCGAGCCCAACTCGCGAGACCTGCCACCTCTACCCGACCGG 584
    |||||
  83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
    |||||
  585 TGCATGATGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCAC 634
    |||||
  100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116

```

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|||||
635 CGGGCGGGCGCGGCTGCACGTGCGGATGCTGGGTGCTGCTGCCCT 684
|||||
116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
|||||
685 GGACTTGGCGGAGGAGCGGGCCACCGCGACGTTCGAGGTACCTGCGCA 734
|||||
133 hrAlaThrGlyAsp 137
|||||
735 CAGCCACGGGGGAC 748

seq_name: N_Geneseq_36:V70595

seq_documentation_block:
ID V70595 standard; cDNA; 751 BP.
AC V70595;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a human multiple tumour suppressor 2 (MTS2) protein.
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key          Location/Qualifiers
FT CDS          335..751
FT FT           /*tag= a
FT FT           /*tag= b
FT FT           /*note= "splice site"
FT US3843756-A.
PD 01-DEC-1998.
PD 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI: 99-044585/04.
DR P-PSDB; W80526.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 6; Fig 11; 80pp; English.
CC The present sequence encodes a human multiple tumour suppressor 2
CC (MTS2) protein. The sequence is homologous to the corresponding
CC murine gene. Primers designed from the gene can be used to design
CC primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;

alignment_scores:
  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101 Percent Identity: 95.652

alignment_block:
  US-09-016-869A-4 x V70595  ..
  Align seg 1/1 to: V70595 from: 1 to: 751

  1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
    |||||
  335 ATGCGCGAGGAGAACAAAGGGCATGCCAGTGGGGCGGCAGCGATGAGG 384
    |||||
  17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSert 33
    |||||
  385 TCTGGCCAGCGCGCGGGGACATAGTGGAGAAAGTGGCAGCTCC 434
    |||||
  33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgAla 49
    |||||
  435 TGGAAAGCGCGCGGATGCCAACAGGAGTCAACCGTTTCGGGAGCGCGG 484
    |||||
  50 IlegInValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
    |||||
  485 ATCCAGGTCTATGATGATGGGCGAGCGCGCGTGGCGAGCTGCTGCT 534
    |||||

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alignment_scores:
  Quality: 554.00      Length: 134
  Ratio: 4.541        Gaps: 2
  Percent Similarity: 91.045  Percent Identity: 84.328

alignment_block:
  US-09-016-869A-4 x T02964

  Align seg 1/1 to: T02964 from: 1 to: 580

      5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr... 20
      82 GACAGGGGATG...TTGGCGCGGACAGTGCAGCGGGCTGGCCACCGC 128
      21 ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
      129 CGCGCGCGGGGCAAGTGGAGACAGGTGGCGGAGCTCTTGGGAAGCGGCG 178
      37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
      179 CAGATCCCAACCCCTGACACCGCTTCGGGAGCGGCCCAATCCAGGTCATG 228
      54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyValAc 70
      229 ATGATGGGCGAGCGCCAGGTGGCAGAGCTGCTGCTCCAGGAGCAGA 278
      70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
      279 ACCCAACTGCGCGGACCTTGCACACCTTACCAGACCTGTGCAGCAGCAG 328
      87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
      329 CTCGGGAGAGCTTCTGGACACGCTTGTGCTGCACCGGCGGCGGCG 378
      104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaCl 120
      379 CGGTGGATGTGTGACCGCTGGGCGGCGCTGCGGTAGACTTGGCTGA 428
      120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137
      429 AGAGCAGGGCCACCGTGACATGGCAGGTATCTGCACGCTGCCACTGGAG 478
      137 sp 137
      479 AT 480

seq_name: N_Geneseq_36:V70624

seq_documentation_block:
  ID V70624 standard; cDNA; 393 BP.
  DT 03-FEB-1999 (first entry)
  DE Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence.
  KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer; ss.
  OS Mus musculus.
  FH Key Location/Qualifiers
  FT CDS 1..393
  FT FT /*tag= a
  FT misc_feature 132..133
  FT FT /*tag= b
  FT FT /*note= "splice site"
  FT US5843756-A.
  PN 01-DEC-1998.
  PD 28-JUL-1995; 058735.
  PR 28-JUL-1995; US-508735.
  PR 07-JUN-1995; US-487033.
  PA (MIRI-) MIRIAD GENETICS INC.
  PI Jiang P, Kamb A, Stone S;
  DR WPI; 99-044585/04.
  DR P-PSDB; W70823.
  PT Mouse multiple tumour suppressor gene segment - useful for primer design

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PS Example 7; Fig 18; 80pp; English.
CC The present sequence encodes mouse multiple tumour suppressor 2
CC (MTS2) gene. The MTS1 gene can be used to design primers to
CC detect abnormalities i.e. polymorphisms which may predispose
CC towards malignancies such as melanoma, leukaemia, astrocytoma,
CC lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;

alignment_scores:
  Quality: 545.50      Length: 128
  Ratio: 4.623        Gaps: 1
  Percent Similarity: 92.188  Percent Identity: 85.156

alignment_block:
  US-09-016-869A-4 x V70624

  Align seg 1/1 to: V70624 from: 1 to: 393

      11 GlyGlyGlySerAspGluGlyLeuAlaThr...ProAlaArgGlyLeuVa 26
      7 GCGGCGACGAGTGCAGCGGGCTGCGCACCGCGCGGCGGGGGCAAGT 56
      26 lGluLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyVala 43
      57 GGAGACGGTGGCGCAACTCTCTGGAAGCGGCGCAGATCCCAACGCCCTGA 106
      43 snArgPheGlyArgAlaIleGlnValMetMetMetGlySerAlaArg 59
      107 ACCGCTCGGAGGCGCCCAATCCAGGTATGATGATGGCGGCGGCCAG 156
      60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76
      157 GTGCGAGAGCTGCTGCTGCTCCAGGAGCAGACCCAACTGCGCGGACCC 206
      76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA 93
      207 TGCACACCTTACCAGACCTGTGCACGACGCGCAGCTCGGGAGGCTTCCTGG 256
      93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
      257 ACAGCTTGTGCTGCTGCACCGGCGGCGGCGGCTGGATGTGTGTGAC 306
      110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126
      307 GCCTGGGCGGCGCTGCGGTAGACTTGGCTGAAGACGAGCGGCCACCGTGA 356
      126 pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
      357 CATTCGAGGATATCTGCACGCTGCCACTGGAGAT 390

seq_name: N_Geneseq_36:X26232

seq_documentation_block:
  ID X26232 standard; DNA; 1073 BP.
  AC X26232;
  DT 25-MAY-1999 (first entry)
  DE Truncated p27/p16 fusion protein encoding DNA.
  KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
  KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
  KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
  KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
  KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
  KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
  KW tachycardia; human; p27; p16; truncated; ss.
  OS Homo sapiens.
  PN W0906540-A2.
  PD 11-FEB-1999.
  PR 29-JUL-1998; U15759.
  PR 29-JUL-1997; US-902572.
  PA (MITO-) MITOTIX INC.
  PI Beach DH, Gyuris J, Lamphere L;

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DR WPI; 99-153770/13.
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60; Page 83-84; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/p16 fusion
CC protein.
SQ Sequence 1073 BP; 215 A; 317 C; 388 G; 153 T;

alignment_scores:
  Quality: 513.00      Length: 158
  Ratio: 4.347        Gaps: 2
  Percent Similarity: 74.684      Percent Identity: 70.253

alignment_block:
US-09-016-869A-4 x X26232 ..
Align seg 1/1 to: X26232 from: 1 to: 1073

3 GluGluAsnLysGlyMetProSerGlyGlySerAspGluGly..... 17
||||| : : : : : : : : : : : : : : : : : : : :
526 GAAGAAAATGTTTCAGACGGTGTGGCGGGGCGACGGGGTGGCGGTTTC 575
17 .....

576 CGCGCGGGGTGGATCCGTCGAGGATCCGGCGGGGAGCAGCATGGAGC 625
18 .....LeuAlaThr...ProAlaArgGlyLeuValGluLys 28
||||| : : : : : : : : : : : : : : : : : : : :
626 CTTCCGGCTGACTGGTCCACCGCGCGCGCGGGTGGGTAGAGGAG 675
29 ValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyValAsnArgPh 45
||||| : : : : : : : : : : : : : : : : : : : :
676 GTGCGGCGCTGCTGGAGCGGGGGGCGCTGCCCAACGCACCGAATAGTTA 725
45 eGlyArgArgAlaIleGlnValMetMetMetGlySerAlaArgValAlaG 62
:||||| : : : : : : : : : : : : : : : : : : : :
726 CGGTGCGAGCGCGATCCAGGTGATGATGATGGCAGCGCCCGAGTGGCGG 775
62 luLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThr 78
||||| : : : : : : : : : : : : : : : : : : : :
776 AGCTGCTGCTCTCCACGGCGCGAGCCCAACTGCGCGGACCCCGCCACT 825
79 LeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLe 95
||||| : : : : : : : : : : : : : : : : : : : :
826 CTCACCGACCGGTGCACAGCGCTGCCCGGAGGGGCTTCCTGGACAGCT 875
95 uValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpG 112
||||| : : : : : : : : : : : : : : : : : : : :
876 GGTGGTGTGTCACCGCGCGGGCGGGCGTGGAGCTGGCGGATGCTCTGGG 925
112 lyArgLeuProValAspLeuAlaGluArgGlyHisArgAspValAla 128
||||| : : : : : : : : : : : : : : : : : : : :
926 GCCCTCTGCCGCTGGAGCTGGCTGAGGAGCTGGGCCATCGCGATGTCGA 975
129 GlyTyrLeuArgThrAlaThrGly 136
```

```
||||| : : : : : : : : : : : : : : : : : : : :
976 CGGTACTCGCGCGCTGCGGGG 999
seq_name: N_Geneseq_36:X26234
seq_documentation_block:
ID X26234 standard; DNA; 782 BP.
AC X26234;
DE Truncated p27/p16 fusion protein encoding DNA.
KW Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
KW CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne;
KW intracellular; transcellular; transcytosis; vascular wound; repair; hair;
KW smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated; ss.
OS Homo sapiens.
PN WO906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI; 99-153770/13.
DR P-PSDB; W95106.
PT Fusion and chimaeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60; Page 85; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCs to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/p16 fusion
CC protein.
SQ Sequence 782 BP; 137 A; 236 C; 295 G; 114 T;

alignment_scores:
  Quality: 509.00      Length: 144
  Ratio: 4.426        Gaps: 2
  Percent Similarity: 79.861      Percent Identity: 75.694

alignment_block:
US-09-016-869A-4 x X26234 ..
Align seg 1/1 to: X26234 from: 1 to: 782

7 GlyMetProSerGlyGlySerAspGluGly..... 17
||||| : : : : : : : : : : : : : : : : : : : :
277 GCGGTTCCGCGGGGTGGATCCGTCGAGGATCCGCGGGGGGAGCAG 326
18 .....LeuAlaThr...ProAlaArgGlyLeuV 26
||||| : : : : : : : : : : : : : : : : : : : :
327 CATGAGACCTTCGCTGACTGGCTGGCCACGCGCGCGGGTTCGGG 376
26 alGluLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyVal 42
||||| : : : : : : : : : : : : : : : : : : : :
377 TAGAGGAGGTGCGGGCGCTGCTGGAGCGGGGGCGCTGCCCAACGACCG 426
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43 AsnArgPheGlyArgAlaIleGlnValMetMetMetGlySerAlaAr 59
|||||
427 AATAGTTACGGTCGGAGCGCATGAGTATGATGGGAGCGCGCG 476
59 gValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAsp 76
|||||
477 ATGGGGAGCTGCTGCTCCAGCGCGGAGCCCACTCGCGGACC 526
76 roAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeu 92
|||||
527 CGGCCACTCTCACCCGACCGTGCAGACGCTGCCGGGAGGCTCCG 576
93 AspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAs 109
577 GACACGCTGGTGGTGCACCGCGCGCGGCGGCTGGAGCTGCGCGA 626
109 pAlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgA 126
627 TGCTGGGGCGCTGCTGCCGCTGGACCTGGCTGAGGAGCTGGGCCATCGCG 676
126 spValAlaGlyTyrLeuArgThrAlaThrGly 136
677 ATGTGCGACGGTACCTGCGCGGCTGCGGG 708
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seq_name: N_Geneseq_36:V11238

seq_documentation_block:

ID V11238 standard; cdna; 471 BP.

AC V11238;

DE 15-JUL-1998 (first entry)

DE Human MTS1 cDNA.

KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS

FT 1. 471

FT /*tag= a

FT /product= MTS1

FT /note= "multiple tumour suppressor"

FN US5739027-A.

PD 14-APR-1998.

PF 07-JUN-1995; 487033.

PR 07-JUN-1995; US-487033.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-250421/22.

DR P-PSDB; W40524.

PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are

PT useful for the diagnosis of cancers related to MTS1E1-beta

PT mutation(s) and their treatment

PS Disclosure; Column 61-62; 72pp; English.

CC This cDNA sequence encodes a human multiple tumour suppression protein,
CC MTS1. The MTS gene locus is also referred to as the familial melanoma
CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations
CC in MTS genes can be used in the diagnosis of predisposition to cancers,
CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
CC ovary, uterus, testis, kidney, stomach and rectum.

SQ Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;

alignment_scores:

Quality: 506.50

Ratio: 4.404

Percent Similarity: 86.466

Percent Identity: 80.451

alignment_block:

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US-09-016-869A-4 x V11238
Align seg 1/1 to: V11238 from: 1 to: 471
9 ProSerGlyGlySerAspGlu.....GlyLeuAlaThr... 20
|||||
7 CGCGGGGGGGAGCAGCATGAGCGCTTCGGCTGACTGGCTGGCCACGGC 56
21 ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||
57 CGCGCCCGGGGTGGGTAGAGAGGTGCGGGCGCTGCTGGAGCGGGGG 106
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
|||||
107 CGCTCCCAACGACCGCAATAGTTACGGTCGAGGCGCATCCAGGTCATG 156
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
|||||
157 ATGATGGCAGCGCCGAGTGGCGGAGCTGCTGCTCCAGCGCGCGGA 206
70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
207 GCCCAACTGCGCGACCCCGCACCTCTCACCGACCGCTGCACGACGCTG 256
87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
257 CCGGGAGGGCTTCCTGCACGCTGGTGGTGCACCGCGCGCGGGCGG 306
104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
307 CGCTGGAGCGCGCGAGTCCCTGGGGCGCTGCGCCGTGGACCTGGCTGA 356
120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
357 GGAGCTGGGCATCGCATGTGCGACGCTACCTGCGCGCGGCTGCGGGG 405
```

seq_name: N_Geneseq_36:V53819

seq_documentation_block:

ID V53819 standard; cdna; 471 BP.

AC V53819;

DT 04-DEC-1998 (first entry)

DE Nucleotide sequence of the CDS of the multiple tumour suppressor 1.

KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;

KW somatic mutation; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS

FT 1. 471

FT /*tag= a

FT /product= "human MTS-1"

FN US5801236-A.

PD 01-SEP-1998.

PF 07-JUN-1995; 480810.

PR 07-JUN-1995; US-480810.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI; 98-494842/42.

DR P-PSDB; W74549.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -

PT useful as hybridisation probes, primers and recombinant production

PT of MTS in the diagnosis and treatment of cancers related to MTS

PT mutation(s)

PS Claim 1; Column 61-62; 73pp; English.

CC This is the nucleotide sequence of the multiple tumour suppressor 1

CC (MTS-1) gene, used in the method of the invention. The MTS gene

CC is useful in the diagnosis and prognosis of human cancer, e.g. by

CC standard nucleic hybridisation techniques, of patient samples. The

KW cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
KW tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
KW tachycardia; human; p27; p16; truncated; ss.
OS Homo sapiens.
PN WO9906540-A2.
PD 11-FEB-1999.
PF 29-JUL-1998; U15759.
PR 29-JUL-1997; US-902572.
PA (MITO-) MITOTIX INC.
PI Beach DH, Gyuris J, Lamphere L;
DR WPI: 99-153770/13.
DR P-PSDB: W95105.
PT Fusion and chimeric proteins including cyclin-dependent kinase
PT binding motif - used for regulation of cell proliferation and
PT differentiation, for treatment of, e.g. vascular injury, cancers,
PT fibrosis and neurodegeneration
PS Claim 60; Page 84-85; 88pp; English.
CC The invention relates to novel inhibitors of cyclin-dependent kinases
CC (CDKs), particularly CDK/cyclin complexes. It provides a recombinant
CC transfection system (A) that comprises: (i) first gene construct
CC comprising a sequence encoding an inhibitory polypeptide containing at
CC least one CDK-binding motif for binding and inhibiting activity of a CDK,
CC linked to a transcription regulator functional in eukaryotic cells; (ii)
CC second gene construct comprising a sequence encoding a polypeptide that
CC promotes endothelialisation, and (iii) a gene delivery composition for
CC delivering the GCS to a cell for transfection. Also provided are nucleic
CC acids encoding a fusion protein (FP) containing: (i) a therapeutic
CC polypeptide sequence (TP) from an intracellular protein that alters a
CC cellular process when FP enters the cell, and (ii) a transcellular
CC polypeptide sequence (TCP) that promotes transcytosis of FP. The FP
CC consists of at least one CDK-binding motif and a TCP. See X26220 for
CC detailed uses of the recombinant transfection system. The present
CC sequence represents a DNA encoding a human truncated p27/p16 fusion
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Date: Jul 21, 2000 8:07 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannan, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 328..738
; US-08-306-511A-3

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; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,274
; FILING DATE: 15-JULY-1997
; CLASSIFICATION: 800
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; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEPTEMBER-1994
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; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
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; FILING DATE: 14-APRIL-1994
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; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOVEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DECEMBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCTOBER-1992
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; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 328..738
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Ratio: 5.234 Gaps: 0
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; Patent No. 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
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APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
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LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
; US-08-487-033-15
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  Quality: 667.50      Length: 138
  Ratio: 4.981        Gaps: 1
  Percent Similarity: 97.101  Percent Identity: 95.652

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; Patent No. 5801236
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
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; Sequence 15, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
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; Sequence 15, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,083
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751

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; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 335..751
US-08-486-047-15

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Quality: 667.50 Length: 138
Ratio: 4.981 Gaps: 1
Percent Similarity: 97.101 Percent Identity: 95.652

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33 rpGluAlaGlyAlaAspProAsnGlyValAsnA-gPheGlyArgAla 49
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735 CAGCCACGGGGGAC 748
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Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/480,810
APPLICATION NUMBER: 08/480,810
FILING DATE:
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FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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FILING DATE: 18-MAR-1994
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APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 335..751
US-09-120-130-15

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Percent Similarity: 97.101 Percent Identity: 95.652

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; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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1 FILING DATE: 02-JAN-1996
2 CLASSIFICATION: 435
3 PRIOR APPLICATION NUMBER: US 08/497,214
4 FILING DATE: 30-JUN-1995
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/346,147
7 FILING DATE: 29-NOV-1994
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 08/306,511
10 FILING DATE: 14-SEP-1994
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/248,812
13 FILING DATE: 23-MAY-1994
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/227,371
16 FILING DATE: 14-APR-1994
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 08/154,915
19 FILING DATE: 18-NOV-1993
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 07/991,997
22 FILING DATE: 17-DEC-1992
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Vincent, Matthew P.
25 REGISTRATION NUMBER: 36,709
26 REFERENCE/DOCKET NUMBER: MIV-071.06
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (617) 832-1299
29 TELEFAX: (617) 832-7000
30 INFORMATION FOR SEQ ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 850 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: both
35 TOPOLOGY: linear
36 MOLECULE TYPE: CDNA
37 FEATURE:
38 NAME/KEY: CDS
39 LOCATION: 338..751
40 US-08-581-918A-3

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; GENERAL INFORMATION:
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; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Therto
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; COMPUTER READABLE FORM:
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; LENGTH: 850 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 338..751
; PCT-US95-04636-3

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Ratio: 4.981 Gaps: 1
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US-09-016-869A-4 x PCT-US95-04636-3 ..

Align seg 1/1 to: PCT-US95-04636-3 from: 1 to: 850

1 MetArgGluGluAsnLysGlyMetProSerGlyGlySerAspGluG1 17
|||||
338 ATGCGCGAGGAGACACAGGCGATGCCAGTGGGGCGGCGACGATGAGG 387
|||||


```
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: WordPad
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/581,918A
;; FILING DATE: 02-JAN-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/497,214
;; FILING DATE: 30-JUN-1995
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/346,147
;; FILING DATE: 29-NOV-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/306,511
;; FILING DATE: 14-SEP-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/248,812
;; FILING DATE: 25-MAY-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/227,371
;; FILING DATE: 14-APR-1994
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 08/154,915
;; FILING DATE: 18-NOV-1993
;; APPLICATION DATA:
;; APPLICATION NUMBER: US 07/991,997
;; FILING DATE: 17-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MIV-071.06
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 832-1299
;; TELEFAX: (617) 832-7000
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 580 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 91..480
US-09-581-918A-7
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alignment_scores:
  Quality: 554.00      Length: 134
  Ratio: 4.541        Gaps: 2
Percent Similarity: 91.045 , Percent Identity: 84.328

alignment_block:
US-09-016-869A-4 x US-08-581-918A-7 ..

Align seg 1/1 to: US-08-581-918A-7 from: 1 to: 580

5 AsnLysGlyMetProSerGlyGlySerAspGluGlyLeuAlaThr... 20
:::|||||  |||:::|||||  |||:::|||||  |||:::|||||
82 GACAGGGGATG...TTGGCGGCGAGTGTGACCGCGGCTGGCCACCGC 128
21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
129 CCGCGCGCGGGGCAAGTGGAGCAGGTGGCGGAGCTCTGGGAAGCGGCG 178
37 laAspProAsnGlyValAsnArgPheGlyArgAlaIleGlnValMet 53
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
179 CAGATCCCAACACCGCTTCGACCGCTTCGGGAGCGGCCAATCCAGGTGATG 228
54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaG1 70
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61 agluLeuLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaT 78
 516 GGAGCTGCTGCTCCACGGCGGAGGCCCACTGCGCNGACCCGCCA 467
 78 hrLeuThrArgProValHisAspAlaAaArgGluGlyPheLeuAspThr 94
 466 CTCTCACCGACCGCTGCACGAGTGCCTCCGCGAGGCTCTCTGCACAGC 417
 95 LeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTr 111
 416 CTGTGGTGTCTGCACCGCGCGGCGCGCTGGACGTGCGGATGCTGTG 367
 111 pGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAspValA 128
 366 GGGCGCTGTGCGCGTGCCTGCTGAGGAGTGGCGCATCGGATGCTG 317
 128 laGlyTyrLeuArgThrAlaThrGly 136
 316 CACGGTACTGCGCGGCTGCGGGG 291

seq_name: gb_est41:AW328496

seq_documentation_block: 648 bp mRNA EST 28-JAN-2000
 LOCUS AW328496 ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
 DEFINITION sequence.
 ACCESSION AW328496
 VERSION AW328496.1 GI:6798992
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 JOURNAL
 COMMENT On Apr 7, 1998 this sequence version replaced gi:3036295.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Edge Biosystems
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Plate: LLCM0030 row: 0 column: 24
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers

FEATURES

source
 1. 648
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847599"
 /clone_lib="NIH_MGC_4"
 /cell_line="MGC1"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Cervix; Vector: pOTB7a; Site_1: Scel;
 Site_2: CeuI; cDNA made by oligo-dT priming.
 Directionally cloned into CeuI/Scel sites using the
 following 5' adaptor: taactatacggctcctaagtagcga and 3'
 adaptor: ttctatacctcttcgcacccacataaa. Average
 insert size 900 bp. Library prepared by Edge Biosystems."

BASE COUNT 127 a 200 c 196 g 123 t 2 others
 ORIGIN

alignment_scores:

Quality: 423.00 Length: 101
 Ratio: 4.648 Gaps: 1
 Percent Similarity: 90.099 Percent Identity: 86.139

alignment_block:

US-09-016-869A-4 x AW328496 ..

Align seg 1/1 to: AW328496 from: 1 to: 648

36 GlyAlaAspProAsnGlyValAsnArgPheGlyArgAlaAlaGlnVa 52
 |||||
 70 GGAGCCAGCGTCTAGGCGCAGCAGCGCTTC.....CTAGAAGACCCAGGT 113
 |||||
 52 lmeMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyA 69
 |||||
 114 CATGATGATGGCGAGCCCGAGTGGGAGCTGCTGCTGCTCCACGGCG 163
 |||||
 69 laGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisasp 85
 |||||
 164 CGGAGCCCAACTGCGCGCAGCCCGCCACTCTCACCCGACCGCTGCACGAC 213
 |||||
 86 AlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGl 102
 |||||
 214 GCTGCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGACCGGCGCGG 263
 |||||
 102 yAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuA 119
 |||||
 264 GCGCGGCTGACGCTGCGCATGCTGGGCGGCTGCTGCCGTGGACCTGG 313
 |||||
 119 laGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThr 135
 |||||
 314 CTGAGGAGCTGGCGCATCGCATGTCGACGGTACCTGCGGCGGCTGCG 363
 |||||
 136 Gly 136
 |||||
 364 GGG 366

seq_name: gb_est26:AI871381

seq_documentation_block: 590 bp mRNA EST 07-MAR-2000
 LOCUS AI871381 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3'
 DEFINITION similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
 ; mRNA sequence.
 ACCESSION AI871381
 VERSION AI871381.1 GI:5545430
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 590)
 NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTGP), Tumor Gene Index
 Unpublished (1998)
 COMMENT On Oct 30, 1998 this sequence version replaced gi:3813427.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 845 Std Error: 0.00
 Seq primer: -400P from G1bco
 High quality sequence stop: 444.
 Location/Qualifiers
 1. .590
 /organism="Homo sapiens"

FEATURES

source
 1. .590
 /organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:2431317"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCCGATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      114 a   158 c   179 g   139 t
ORIGIN

```

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alignment_scores:
  Quality: 420.00      Length: 86
  Ratio: 5.000        Gaps: 0
  Percent Similarity: 97.674  Percent Identity: 95.349

alignment_block:
US-09-016-869A-4 x AI871381/rev ..

Align seg 1/1 to reverse of: AI871381 from: 1 to: 590

51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi 67
|||||
566 CAGGTCATGATGATGGGAGCGCCAGAGTGGCGGAGCTGCTGCTGCCA 517
|||||

67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||

516 CGGCGGGAGCGCAACTCGCGGACCGCCGCACTCTCACCGACCGCTGC 467
|||||

84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||

466 ACGACGCTGCCCGGAGGCGCTCTGGACAGCTGGTGGTGTGCTGCACCGG 417
|||||

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||

416 GCCGGGGCGCGCTGGAGTGGCGGATGCTGGGCGCTGCTGCCGTGGA 367
|||||

117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||

366 CTGGCTGAGGAGCTGGGCCATCGGATGCGCACGCTACCTGCGCGGG 317
|||||

134 laThrGly 136
|||||
316 CTGCGGGG 309

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seq_name: gb_est36:AI870879

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seq_documentation_block:
LOCUS      AI870879      579 bp      mRNA      EST      07-MAR-2000
DEFINITION w177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933 3'
            similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
            ; mRNA sequence.

```

```

ACCESSION  AI870879
VERSION    AI870879.1 GI:5544847
KEYWORDS  EST.
SOURCE    human.

```

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 579)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

JOURNAL

Unpublished (1998)

COMMENT On May 18, 1998 this sequence version replaced gi:3136959.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 819 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 474.

FEATURES

Location/Qualifiers

1..579

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2430933"

/clone_lib="NCI_CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAAGTGGAGCGCCGATAGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 113 a 157 c 182 g 127 t

ORIGIN

alignment_scores:

Quality: 408.00 Length: 86

Ratio: 4.976 Gaps: 0

Percent similarity: 95.349 Percent Identity: 93.023

alignment_block:

US-09-016-869A-4 x AI870879/rev ..

Align seg 1/1 to reverse of: AI870879 from: 1 to: 579

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51 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67
|||||
555 CAGGTCATGATGATGGGAGCGCCGAGTGGCGGAGCTGCTGCTCCA 506
|||||

67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||

505 CGGCGGGAGCGCAACTCGCGGACCGCCGCACTCTCACCGACCGCTGC 456
|||||

84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||

455 ACGACGCTGCCCGGAGGCGCTCTGGACAGCTGGTGGTGTGCTGCACCGG 406
|||||

101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||

405 GCCGGGGCGGGCTGGACGTGGCGGATGCTGGGGCGCTGCGCGTGA 356
|||||

117 pLeuAlaGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||

355 CTGGCTGAGGAGCTGGGCCATCGGATGCGCACGCTACCTGCGCGGG 306
|||||

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134 laThrGly 136

|||||

305 CTGCGGGG 298

seq_name: gb_est17:AI198233

seq_documentation_block:

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LOCUS      AI198233      579 bp      mRNA      EST      02-DEC-1998
DEFINITION q155d12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3'
            ; contains LTR9.b3 TAR1 TAR1 repetitive element ; , mRNA sequence.
ACCESSION  AI198233
VERSION     AI198233.1 GI:3750839
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 579)
REFERENCE   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGA), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 729 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 459.
FEATURES   Location/Qualifiers
            1..579
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:1860407"
             /clone_lib="NCI_CGAP_Brn25"
             /tissue_type="anaplastic oligodendroglioma"
             /lab_host="DH10B"
             /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTACCATCTGAAGTGGAGCCGCCATAGGTTTTTTTTTTTTTTTTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT 113 a 158 c 177 g 130 t 1 others
ORIGIN
alignment_scores:
  Quality: 400.00 Length: 96
  Ratio: 4.545 Gaps: 1
  Percent Similarity: 91.667 Percent Identity: 84.375
alignment_block:
US-09-016-869a-4 x AI198233/rev ..
Align seg 1/1 to reverse of: AI198233 from: 1 to: 579
41 GlyValAsnArgPheGlyArgAlaIleGlnValMetMetMetGlyse 57
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
579 GGCAGCAGCGCTCTAGAAA.....GANCAGGTCATGATGATGGCAG 536
57 rAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysa 74
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
535 CGCCCGAGTGGCGAAGCTGCTGCTGCCACGCGGAGCCCACTGCG 486
74 laAspProAlaThrLeuThrArgProValHisAspAlaArgGluGly 90
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

```

485 CCGACGCCGCCACTCTACCCGACCCGTCGACGACGCTGCCCGGGAGGCG 436
91 PheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspVa 107
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
435 TTCTCGGACACGCTGGTGGTCTGCACCGCGCGGGCGGCTGGACGT 386
107 lArgAspAlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyH 124
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
385 GCGCGATGCTGGGCGCTCTGCCGCTGCACCTGGCTGAGGAGCTGGGCC 336
124 lSArgAspValAlaGlyTrpLeuArgThrAlaThrGly 136
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
335 ATCGCGATGTCGACGCGTACCTGCGCGGCTGCGGGG 298
seq_name: gb_est19:AI362049
seq_documentation_block:
LOCUS      AI362049      580 bp      mRNA      EST      15-FEB-1999
DEFINITION qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3'
            ; similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
            ; , mRNA sequence.
ACCESSION  AI362049
VERSION     AI362049.1 GI:4113670
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 580)
REFERENCE   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGA), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 884 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 321.
FEATURES   Location/Qualifiers
            1..580
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:2014405"
             /clone_lib="NCI_CGAP_Brn23"
             /tissue_type="glioblastoma (pooled)"
             /lab_host="DH10B"
             /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTACCATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT 116 a 160 c 174 g 130 t
ORIGIN
alignment_scores:
  Quality: 399.00 Length: 86
  Ratio: 4.866 Gaps: 0

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Percent Similarity: 95.349 Percent Identity: 91.860

alignment_block:

US-09-016-869A-4 x AI362049/rev ..

Align seg 1/1 to reverse of: AI362049 from: 1 to: 580

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51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuH 67
|||||
556 CAGGTGATGATGGCAGCGCTCGAGTGGCGAGCTGCTGCTGCCA 507
|||||
67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
|||||
506 CGCGCGGAGCCCACTGCGCGAGCTCCGCCACTCACCACCGACGTC 457
|||||
84 IsAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||
456 ACGAGCTGCCCGGAGGCTTCTTGAACACGCTGTGTGTGCACCG 407
|||||
101 AlaGlyAlaArgLeuAspValArgAspAlaThrGlyArgLeuProValAs 117
|||||
406 GCGCGGCGCGCTGACGTGCGGATGCTGGGCGCTCTGCCGTGGA 357
|||||
117 pLeuAlaGluAlaArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
|||||
356 CTGGCTGAGGAGCTGGGCGCATCGGATGTCGACGCTACCTGCGCGCG 307
|||||
134 laThrGly 136
|||||
306 CTGCGGG 299
```

seq_name: gb_est25:AI765096

seq_documentation_block:

LOCUS AI765096 774 bp mRNA EST 21-DEC-1999
DEFINITION w448b08.x1 NCI-CGAP Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 19.1 KDA PROTEIN ; contains
LFR9.b3 MER22 repetitive element ;, mRNA sequence.
ACCESSION AI765096
VERSION AI765096.1 GI:5231605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/Image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.

FEATURES
Source

1..774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI-CGAP Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones IDs 1057416-1061255, and 114584-1145351).
Subcloned by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 153 a 220 c 221 g 179 t 1 others
ORIGIN

alignment_scores:

Quality: 399.00 Length: 117
Ratio: 4.200 Gaps: 2
Percent Similarity: 81.197 Percent Identity: 74.359

alignment_block:

US-09-016-869A-4 x AI765096/rev ..

Align seg 1/1 to reverse of: AI765096 from: 1 to: 774

```
22 AlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyAlaAs 38
|||||
677 GCGCCAGGGGGGGCCCCCGCTGTGGGCCATCGTGTATGCTATTGAGGA 628
|||||
38 pProAsn.....GlyValAsnArgPheGlyArgAlaIleGlnValM 53
|||||
627 GCCAGCGTTTAGGCGCAGCAGCGCTTC.....CTAGAAGACCAGGTCA 584
|||||
53 etMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAla 69
|||||
583 TGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGGCGCG 534
|||||
70 GluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAl 86
|||||
533 GAGCCCAATTGGCGCGACCCGCCACTTTCACCCAGCCGTCGACGACGC 484
|||||
86 aAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyA 103
|||||
483 TGCCCGGGAGGGCTTCCTGGACACGCTGGTGTGTGCACGGCGCGGG 434
|||||
103 laArgLeuAspValArgAspAlaThrGlyArgLeuProValAspLeuAla 119
|||||
433 CGCGCTGAGCAGTGGCAATGCTGGGCGCGCTCTGCCGTGGACCTGGCT 384
|||||
120 GluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGl 136
|||||
383 GAGGAGCTGGGCCATCGCGATGTCGCCGGTACCTGCGCGCGGCTTCGG 334
```

136 y 136

333 g 333

seq_name: gb_gss7:AQ496105

seq_documentation_block:

LOCUS AQ496105 614 bp DNA GSS 28-APR-1999
DEFINITION HS.5075.A1.F12.T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-651 Col-23 Row-K, genomic survey sequence.
ACCESSION AQ496105

VERSION AQ496105.1 GI:4696228

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

```

TITLE      Sequence-tagged connectors: A sequence approach to mapping and
           scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    On Dec 15, 1999 this sequence version replaced gi:4575297.
           Contact: Mahairas GG, Wallace JC, Hood L
           High Throughput Sequencing Center
           University of Washington
           401 Queen Anne Avenue North, Seattle, WA 98109, USA
           Tel: (206) 616-3618
           Fax: (206) 616-3887
           Email: jwallace@u.washington.edu
           Clones are derived from the human BAC library RPCI-11. For BAC
           library availability, please contact Pieter de Jong
           (pieter@dejong.med.buffalo.edu). Clones may be purchased from
           BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
           or from Resear h Genetics (info@resgen.com). BAC end Web Server:
           http://www.htsc.washington.edu
           Plate: 651 row: K column: 23
           Seq primer: 17
           Class: BAC ends
           High quality sequence stop: 614.
FEATURES   Location/Qualifiers
            1..614
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="Plate=651 Col=23 Row=K"
             /clone_lib="RPCI-11 Human Male BAC Library"
             /sex="male"
             /note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;
             Male blood DNA was isolated from one randomly chosen donor
             and partially digested with a combination of EcoRI and
             EcoRI Methylase. Size selected DNA was cloned into the
             pBACe3.6 vector at EcoRI sites"
BASE COUNT      117 a 182 c 171 g 133 t 11 others
ORIGIN
alignment_scores
  Quality: 391.00      Length: 86
  Ratio: 4.827      Gaps: 0
  Percent Similarity: 94.186      Percent Identity: 89.535
alignment_block
US-09-016-869A-4 x A0496105 ..
Align seg 1/1 to: A0496105 from: 1 to: 614
51  GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi 67
|||||
291 CAAGTCATGATGATGGCACCGCCGCGAGTGGCGAGCTGCTGCTCCA 340
|||||
67  sGlyAlaGluProAspCysAlaAspProAlaThrLeuThrArgProValH 84
|||||
341 CGGGGGGAGCCCACTGCGCCGACCCCGCCACTTCACCCACCGGTGC 390
|||||
84  isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
|||||
391 ACACGCTGCGCGGAGGGTCTCTGACACACTGGTGTGTCGACCGG 440
|||||
101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
|||||
441 GCGGGGGCGGCTGGACGTGCGTATGCTGGGGCGCTGCTGCCGTGGA 490
|||||
117 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThra 134
|||||
491 CTGTGCTGAGGAGCTGGGCAATCTCGATGTTACAGGTACCTGCGGCGG 540
|||||
134 laThrGly 136
541 ATCGGGGG 548
seq_name: gb_est19:AI363262

```

seq_documentation_block:

LOCUS AI363262 708 bp mRNA EST 16-FEB-1999
 DEFINITION qv56f03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3' similar to TR:Q13195 Q13195 P16INK4/WTSL [2] TR:Q13399 ; contains LTR9.b3 TAR1 repetitive element ; , mRNA sequence.

ACCESSION AI363262
 VERSION AI363262.1 GI:4114883

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 708)

AUTHORS

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BRGAP), Tumor Gene Index

JOURNAL

Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,

Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 872 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 394.

FEATURES

Location/Qualifiers

1..708

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2016029"

/clone_lib="NCI_CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH108"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCAATCTGAGTGGCGGCATATCTTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 137 a 210 c 219 g 140 t 2 others

ORIGIN

alignment_scores:

Quality: 390.00 Length: 96

Ratio: 4.588 Gaps: 1

Percent Similarity: 88.542 Percent Identity: 83.333

alignment_block:

US-09-016-869A-4 x AI363262/rev ..

Align seg 1/1 to reverse of: AI363262 from: 1 to: 708

41 GlyValAsnArgPheGlyArgArgAlaIleGlnValMetMetGlyse 57

|||||

564 GGCAGCAGCCGCTTC.....CTAGAAGANCAGTTCATGATGATGCAAG 521

57 rAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysa 74

|||||

520 CGCCCGAGTGGCGAGCTGCTGCTCCCGGGCGGCGGCACTGCG 471

```

74 laaspProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGly 90
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
470 ACGACCCGCCCAACTCTCACCGACCGTGCACGCTGCCGCCGGAGGC 421
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
91 PheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspVa 107
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
420 TTCCTGGACAGCTGGTGGTCTGCACCGCGCGCGCGCGCTGGACGT 371
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
107 lArgAspAlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyH 124
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
370 GCGCGATCGCTGGCGCGCTCTGCCGTGGACCTGGCTGAGGAGTGGGCC 321
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
124 lArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
320 ATCCGATGTCGACGGTACCTGCGCGCGCTGCGGG 283
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

```

seq_name: gb_est25:A1817709

seq_documentation_block: 729 bp mRNA EST 21-DEC-1999
LOCUS A1817709
DEFINITION wk25cl1.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA sequence.

ACCESSION A1817709
VERSION A1817709.1 GI:5436788
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 729)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index

JOURNAL Unpublished (1998)

COMMENT On Apr 7, 1998 this sequence version replaced gi:3035534.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 848 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence step: 468.

Location/Qualifiers

1..729

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2413364"

/tissue_type="NCI_CGAP_Brn25"

/lab_host="DH108"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 141 a 214 c 226 g 143 t 5 others

ORIGIN

alignment_scores:
Quality: 384.00 Length: 127
Ratio: 3.959 Gaps: 2
Percent Similarity: 76.378 Percent Identity: 69.291

alignment_block:

US-09-016-869a-4 x A1817709/rev ..

Align seg 1/1 to reverse of: A1817709 from: 1 to: 729

32 SerTrpGluAlaGlyAlaAspProAsnGlyVal...AsnArgPheGlyAr 47
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

677 TCGTGGTTTCATCCCGCGNGCTCACGGGAGTGGGCGAGCCCGAGGGCG 628
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

47 gArgAlaIle..... 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

627 CCGCGNGCTGTGGCCCTCGTCTACTGAGAGCCCGAGCGCTAGG 578
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

51GlnValMetMetMetGlySerAlaArg 59
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

577 GCAGCAGCCGCTCTCTAGAACACCGTCTATGATGAT.GGCAGCGCCGAA 529
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

60 ValAlaGluLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

528 GTGGCGAGGCTGCTGCTCCACGGCGCGGACCACTGCGCGCGACNC 479
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeu 93
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

478 CGCCACACTCTCACCGACCCCTGCACGACGCTGCCCGGAGGCTTCCTGG 429
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

428 ACACGCTGGTGGTCTCACCGCGCGCGGCGGCTGGACGTGCGCGAT 379
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

378 GCTTGGGCGCGTCTGCCGCTGGACCTGCTGAGGAGCTGGCCATCGCA 329
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

126 pValAlaGlyTyrLeuArgThrAlaThrGly 136
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

328 TGTGCGACGGTACCTGCGCGCGGCTGCGGG 298

seq_name: gb_est27:A1954684

seq_documentation_block:

LOCUS A1954684 563 bp mRNA EST 08-MAR-2000

DEFINITION wq34hl2.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:247323 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A ;, mRNA sequence.

ACCESSION A1954684

VERSION A1954684.1 GI:5746994

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 613 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 460.
Location/Qualifiers
1. .563

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2473223"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 112 a 138 c 169 g 124 t
ORIGIN

alignment_scores:

Quality: 381.00 Length: 90
Ratio: 4.590 Gaps: 0
Percent Similarity: 92.222 Percent Identity: 88.889

alignment_block:

US-09-016-869A-4 x AI954684/rev ..

Align seg 1/1 to reverse of: AI954684 from: 1 to: 563

47 ArgArgAlaileInValMetMetMetGlySerAlaArgValAlaGluLe 63
|||||
::: |||||
563 AGGCCAAATGATAGGGTCTATGATATGGCAGCGCCGAGTGGCGGAGCT 514
63 uLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeu 80
|||||
|||||
513 GCTGCTGCTCCACGGCGGGAGGCCCACTG.CCCGACCCGCCCACTCTCA 465
80 hrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLeuVal 96
|||||
|||||
464 CCCGACCCGTGCACACGCTGCCCGGGAGGGCTTCTGGACACGCTGGT 415
97 ValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyAr 113
|||||
|||||
414 GTGCTGCACCGCGCGGGCGGGCTGGACGTGCGCGATGCTGGGGCGG 365
113 gLeuProValAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyT 130
|||||
|||||
364 TCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCATGCGCACGCT 315
130 yLeuArgThrAlaThrGly 136
|||||
|||||
314 ACCTGCGCGGCTGCGGGG 295

seq_name: gb_est26:AI885362

seq_documentation_block:

LOCUS AI885362 528 bp mRNA EST 07-MAR-2000
DEFINITION w192h04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A.; mRNA sequence.

ACCESSION AI885362

VERSION AI885362.1 GI:5590526

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 528)

AUTHORS

TITLE
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTIGAP), Tumor Gene Index

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 626 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 465.

FEATURES

source

1. .528

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="IMAGE:2432407"

/clone_lib="NCI_CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; Double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT

106 a 143 c 165 g 114 t

ORIGIN

alignment_scores:

Quality: 377.00 Length: 77
Ratio: 5.027 Gaps: 0
Percent Similarity: 97.403 Percent Identity: 94.805

alignment_block:

US-09-016-869A-4 x AI885362/rev ..

Align seg 1/1 to reverse of: AI885362 from: 1 to: 528

60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr 76
|||||
|||||
528 GTGCGGAGCTGCTGCTGCTCCACGGCGGGAGCCCACTGCGCGGACCC 479
76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA 93
|||||
|||||
478 CGCCACTCTCACCCGACCGGTGCACGACGCTGCCGGGAGGGCTTCCTGG 429
93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgasp 109
|||||
|||||
428 ACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 379
110 AlaTrpGlyArgLeuProValAspLeuAlaGluArgGlyHisArgAs 126
|||||
|||||
378 GCTTGGGGCGGCTGCGCCCTGGACCTGGCTGGAGAGCTGGGCCATCGCA 329
126 pValAlaGlyTyrLeuArgThrAlaThrGly 136
|||||
|||||
328 TGTGCGACGCTACCTGCGCGGCGCTGCGGGG 298

seq_name: gb_est23:AI633790

```
seq_documentation_block: 531 bp mRNA EST 14-DEC-1999
LOCUS AI633790
DEFINITION tt28610.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242122 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI633790
VERSION AI633790.1 GI:4685120
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 531)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI_CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 623 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 454.
FEATURES
Location/Qualifiers
source
1..531
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tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 107 a 144 c 163 g 116 t 1 others
ORIGIN

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Ratio: 4.973 Gaps: 0
Percent Similarity: 96.154 Percent Identity: 93.590

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US-09-016-869A-4 x AI633790/rev ..
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531 CGATGGCGGAGCTGCTGCTCCACGGCGGAGCCCACTGCGCGGA 482
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75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92
|||||
481 CNCGCCCACTCTCACCCACCGCTGCACGACGCTGCCCGGAGGCGCTCC 432
|||||
92 euAspThrLeuValLeuHisArgAlaGlyAlaArgLeuAspValArg 108
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431 TGGACACGCTGCTGCTGCACCGGGCGGCGGCTGCGCTGCGGC 382
109 AspalatrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisAr 125
|||||
381 GATCGCTGGGGCCGCTCTGCCGCTGGACCTGCTGAGGAGCTGGGCCATCG 332
|||||
125 gAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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331 CGATGTCGACACGCTACCTGCGCGGCTGCGGGG 298
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seq_name: gb_est23:AI638416

seq_documentation_block: 528 bp mRNA EST 14-DEC-1999
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DEFINITION tt31903.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI638416
VERSION AI638416.1 GI:4690650
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 528)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI_CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 462.
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/lab_host="DH10B"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 106 a 143 c 163 g 114 t 2 others
ORIGIN

alignment_scores:
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Ratio: 4.920 Gaps: 0
Percent Similarity: 96.154 Percent Identity: 92.308

alignment_block:
US-09-016-869A-4 x AI638416/rev ..
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 528 CGAGTGGCGAGCTGTGCTGCCAGCGCGGAGCCCAACTGCGNCGA 479
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 75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92
 |
 478 CNGCGCACTCTCACCGACCGCTGACGACGCTGCCGGGAGGCTTCC 429
 |||||
 92 euAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArg 108
 |||||
 428 TGGACAGCTGGTGGTGTCTCACCGCGCGCGGCGGCTGGAGCTGCGC 379
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 109 AspAlaTrpGlyArgLeuProValAspLeuAlaGluGlyHisArg 125
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 378 GATGCTGGGGCGCTGTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 329
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 125 gAspValAlaGlyTyrLeuArgThrAlaThrGly 136
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seq_name: gb_est13:AA909181

seq_documentation_block: 526 bp mRNA EST 10-JUN-1998
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 IMAGE:1523215 3' similar to TR:Q16361 Q16361 CBLL CYCLE NEGATIVE
 REGULATOR BETA FORM ;, mRNA sequence.
 ACCESSION AA909181
 VERSION AA909181
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 526)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT On Apr 7, 1998 this sequence version replaced gi:3034533.
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LILN; contact the
 IMAGE Consortium (info@image.liln.gov) for further information.
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 Seq Primer: -40ml3 fwd. ET from Amersham
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 a modified polylinker; Site.1: Not I; Site.2: Eco RI;
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 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CGAP_GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 882632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

FEATURES
 source

BASE COUNT 82 a 175 c 155 g 113 t 1 others
 ORIGIN

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 Ratio: 4.500 Gaps: 1
 Percent Similarity: 90.698 Percent Identity: 88.372

alignment_block:
 US-09-016-869A-4 x AA909181/rev ..
 Align seg 1/1 to reverse of: AA909181 from: 1 to: 526

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 514 GTCATGATGATGGGAGAGGCTTCCTGGACACGCTGGTGTCTGCACG 465
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 464 GCGGAGAGCCCAACTGGCGCGGACCCGCCACTCTCACCCGACCCGTCAC 415
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 85 AspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAl 101
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 414 GACGCTGCCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGGGC 365
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 101 aGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspL 118
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 364 CGGGGCGCGCTGGACGTCGCGGATGCCCTGGGC.CGTCTGCCCGTGGACC 316
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 118 euAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAla 134
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 135 ThrGly 136
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 265 CGGGGG 260

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:05:24 ; Search time 2513.97 Seconds
(without alignments)
605.555 Million cell updates/sec

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Perfect score: 853
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Gapop 10.0 , Gapext 1.0
Searched: 972840 seqs, 892348106 residues 1945680
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_ba2:*

3: gb_ov:*

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5: gb_pat:*

6: gb_ph:*

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69: gb_htg20:*

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77: gb_htg28:*

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79: gb_htg30:*

80: gb_htg31:*

81: gb_v11:*

82: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	674.4	79.1	713	12	S80650	S80650 p16INK4a-CD
3	672.8	78.9	713	5	I89920	I89920 Sequence 1
4	640	75.0	846	12	MUSP16INK	L76150 Mus musculus
5	640	75.0	849	12	AF044336	AF044336 Mus muscu
6	638.4	74.8	849	12	AF044335	AF044335 Mus muscu
7	382.2	44.8	507	5	AR062814	AR062814 Sequence
8	375	44.0	395	5	AR001335	AR001335 Sequence
9	375	44.0	395	5	AR037515	AR037515 Sequence
10	375	44.0	395	5	AR062795	AR062795 Sequence
11	375	44.0	395	5	I41169	I41169 Sequence 25
12	345	40.4	482	12	MMINK4A02	U66087 Mus musculus
13	339	39.7	339	12	MSU79634	U79634 Mus spratus
14	335.8	39.4	339	12	MMU79632	U79632 Mus musculus
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16	334.2	39.2	339	12	MMU79630	U79630 Mus musculus
17	332.6	39.0	339	12	MMU79631	U79631 Mus musculus
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19	267	31.3	707	12	L81167	L81167 Rattus norv
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21	228.8	26.8	660	11	S78535	S78535 tumor suppl
22	227.6	26.7	905	10	HSU38945	U38945 Human hypot
23	226	26.5	1131	5	AR062785	AR062785 Sequence
24	224.4	26.3	1131	5	AR001325	AR001325 Sequence

25 224.4 26.3 1131 5 AR037505
26 224.4 26.3 1131 5 I41159 Sequence 13
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28 209.4 24.5 4926 12 NMU238890
29 208.6 24.5 540 5 I89921 Sequence 3
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32 185.8 21.8 189 12 NMU45281
33 162.4 19.0 393 5 AR062815
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35 161.4 18.9 300 12 NMU79636
36 161.4 18.9 300 12 NMU79639
37 161.4 18.9 300 12 MSU79637
38 161.4 18.9 439 12 MMINK4B02
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42 159.8 18.7 2590 12 AF015460
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ALIGNMENTS

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DEFINITION L76092.1 GI:1162946
ACCESSION L76092.1
VERSION p19 protein.
KEYWORDS Mus musculus
SOURCE Mus musculus (clone: MARF) cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 713)
AUTHORS Quelle,D.E., Zindy,F., Ashmun,R.A. and Sherr,C.J.
TITLE Alternative reading frames of the INK4a tumor suppressor gene
encode two unrelated proteins capable of inducing cell cycle arrest
JOURNAL Cell 83 (6), 993-1000 (1995)
MEDLINE 96107337
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DB 204 AAGAGGCGCGACCCGGAATCTGGACCAAGGTGATGATGGCAACGTTACGTAGGAGC 263
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DB 684 TTAATAATACATAATAATGCTTTTTT 711
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RESULT 2

LOCUS S80650 713 bp mRNA ROD 02-APR-1996
DEFINITION p16INK4a-CDK4 and CDK6 cyclin D-dependent kinases inhibitor
{alternatively spliced, exon 1 beta and exon 2} [mice, MEL
erythroleukemia cells, mRNA partial, 713 nt].
ACCESSION S80650
VERSION S80650.1 GI:1245977
KEYWORDS
SOURCE Mus sp. MEL erythroleukemia cells.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 713)
AUTHORS Quelle,D.E., Zindy,F., Ashmun,R.A. and Sherr,C.J.
TITLE Alternative reading frames of the INK4a tumor suppressor gene
encode two unrelated proteins capable of inducing cell cycle arrest
JOURNAL Cell 83 (6), 993-1000 (1995)
MEDLINE 96107337
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 174807] from the original journal article.
This sequence comes from Fig. 2.
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43..552
gene

CDS
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This sequence comes from Fig. 2"
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WERPDRRA"
BASE COUNT 133 a 195 c 223 g 162 t
ORIGIN

Query Match 79.1%; Score 674.4; DB 12; Length 713;
Best Local Similarity 99.7%; Pred. No. 2.3e-163;
Matches 686; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GGAGTACAGCAGCGGAGCATGGTCCGAGGTTCTTGGTCACTGTAAAGATTACAGCGCG 60
DB 24 GGAGTACAGCAGCGGAGCATGGTCCGAGGTTCTTGGTCACTGTGAGGATTACAGCGCG 83
QY 61 GGGCCGCCCACTCCAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 120
DB 84 GGGCCGCCCACTCCAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 143
QY 121 GACAGGAGCTGGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 180
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DB 264 CTCCTCTGCTCAACTACGTGCGATGCTGCGGTTCTTGGTCACTGCGAGGACCCCACT 323
QY 301 CGGTGCACGACGCGGAGGCTTCTTGACACGCTGTTGTTGCTGCGAGGGTCTAG 360
DB 324 CGGTGCACGACGCGGAGGCTTCTTGACACGCTGTTGTTGCTGCGAGGGTCTAG 383
QY 361 GGGCTCGGTGGATGTCGCGATGCTGGGGTGCCTGCGCTCGACTTGGCCCAAGAGC 420
DB 384 GGGCTCGGTGGATGTCGCGATGCTGGGGTGCCTGCGCTCGACTTGGCCCAAGAGC 443
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DB 444 GGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGTGCTCTTGTGTTCCGCTG 503
QY 481 GGTGGTCTTTGTACCGCTGGGAAGTTCGCCAGACCGGAGGATAGCTTACGCTCAA 540
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QY 541 GCACGCCCAAGGGCCCTGGAACCTTCGGGGCAATCCCAAGAGCAGAGCTAAATCC -GCCCTC 599
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DB 624 AGCCGCCCTTTTCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCT 683
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DB 684 TTAATAAATACATAAATGCTTTTTT 711

RESULT 3
189920 713 bp DNA PAT 10-AUG-1998
LOCUS

DEFINITION Sequence 1 from patent US 5723313.
ACCESSION 189920
VERSION 189920.1 GI:3409860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 713)
AUTHORS Sherr,C.J. and Quelle,D.E.
TITLE ARF-p19, a novel regulator of the mammalian cell cycle
JOURNAL Patent: US 5723313-A 1 03-MAR-1998;
FEATURES
Location/Qualifiers
Source 1..713
BASE COUNT 133 a 194 c 224 g 162 t
ORIGIN
Query Match 78.9%; Score 672.8; DB 5; Length 713;
Best Local Similarity 99.6%; Pred. No. 6e-163;
Matches 685; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GGAGTACAGCAGCGGAGCATGGTCCGAGGTTCTTGGTCACTGTAAAGATTACAGCGCG 60
DB 24 GGAGTACAGCAGCGGAGCATGGTCCGAGGTTCTTGGTCACTGTGAGGATTACAGCGCG 83
QY 61 GGGCCGCCCACTCCAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 120
DB 84 GGGCCGCCCACTCCAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAG 143
QY 121 GACAGGAGCTGGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 180
DB 144 GACAGGAGCTGGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 203
QY 181 AAGAGGGCCGACCGGAATCCTGGACAGGTGATGATGATGGCAACGTTACGTAGCAG 240
DB 204 AAGAGGGCCGACCGGAATCCTGGACAGGTGATGATGATGGCAACGTTACGTAGCAG 263
QY 241 CTCCTCTGCTCAACTACGTGCGATGCTGCGGTTCTTGGTCACTGCGAGGACCCCACT 300
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QY 301 CGGTGCACGACGCGGAGGCTTCTTGACACGCTGTTGTTGCTGCGAGGGTCTAG 360
DB 324 CGGTGCACGACGCGGAGGCTTCTTGACACGCTGTTGTTGCTGCGAGGGTCTAG 383
QY 361 GGGCTCGGTGGATGTCGCGATGCTGGGGTGCCTGCGCTCGACTTGGCCCAAGAGC 420
DB 384 GGGCTCGGTGGATGTCGCGATGCTGGGGTGCCTGCGCTCGACTTGGCCCAAGAGC 443
QY 421 GGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGTGCTCTTGTGTTCCGCTG 480
DB 444 GGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGTGCTCTTGTGTTCCGCTG 503
QY 481 GGTGGTCTTTGTACCGCTGGGAAGTTCGCCAGACCGGAGGATAGCTTACGCTCAA 540
DB 504 GGTGGTCTTTGTACCGCTGGGAAGTTCGCCAGACCGGAGGATAGCTTACGCTCAA 563
QY 541 GCACGCCCAAGGGCCCTGGAACCTTCGGGGCAATCCCAAGAGCAGAGCTAAATCC -GCCCTC 599
DB 564 GCACGCCCAAGGGCCCTGGAACCTTCGGGGCAATCCCAAGAGCAGAGCTAAATCCCGCCCTC 623
QY 600 AGCCGCCCTTTTCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCT 659
DB 624 AGCCGCCCTTTTCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCT 683
QY 660 TTAATAAATACATAAATGCTTTTTT 687
DB 684 TTAATAAATACATAAATGCTTTTTT 711
RESULT 4
MUSP16INK

LOCUS MUSP16INK 846 bp mRNA ROD 20-JAN-1996
DEFINITION Mus musculus CDK4 and CDK6 inhibitor protein (p16ink4a) mRNA, complete cds.
ACCESSION L76150
VERSION L76150.1 GI:1162948
KEYWORDS CDK4 inhibitor; CDK6 inhibitor.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 846)
AUTHORS Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rehberger,P.A., Trono,D., Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M.
TITLE Cloning and characterization of murine p16INK4a and p15INK4b genes
JOURNAL Oncogene 11 (4), 635-645 (1995)
MEDLINE 95380169
FEATURES
Location/Qualifiers
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Best Local Similarity 98.5%; Pred. No. 1.7e-134;
Matches 646; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 196 GAATCCTGGACAGGTGATGATGGGCAAGTTCAGGTACAGCTCTTCTGCTCAACT 255
Db 191 GTACCCGATTCAGGTGATGATGGGCAAGTTCAGGTACAGCTCTTCTGCTCAACT 250
Qy 256 ACGGTGCAGATTCGAATCGGAGGACCCCACTACCTTCTCCGCCCGGTGCACGACGAG 315
Db 251 ACGGTGCAGATTCGAATCGGAGGACCCCACTACCTTCTCCGCCCGGTGCACGACGAG 310
Qy 316 CGCGGAGAGCTTCCTGGAACAGCTGGTGGTGGTGCACAGGCTCAGGGCTCGGCTGGATG 375
Db 311 CGCGGAGAGCTTCCTGGAACAGCTGGTGGTGGTGCACAGGCTCAGGGCTCGGCTGGATG 370
Qy 376 TCGCGGATCGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 435
Db 371 TCGCGGATCGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 430
Qy 436 TCGTGCATATTTGGTTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 495
Db 431 TCGTGCATATTTGGTTCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 490
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Db 491 CGCTGGGAAGTCCCGCAGACCGAGCGGCATAGCTTCAGTCAAGCAGCGCCAGCGGCC 550
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Db 551 TGGAACTTCGCGGGCAATCCCAAGAGCAGAGCTAAATCCGCTCAGCCCGCTTTTCTT 610

Qy 616 CTTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCTTTAAAAAATACATAAT 675
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Qy 676 AATGCTTTTTCGAATCAGCGGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 735
Db 671 AATGCTTTTTCGAATCAGCGGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
Qy 736 GAGG 795
Db 731 GAGG 790
Qy 796 GGGGAATATGGCTGGATGTTTAAAAAATAAATAAAGATACATTTTAAAAATGTC 851
Db 791 GGGGAATATGGCTGGATGTTTAAAAAATAAATAAAGATACATTTTAAAAATGTC 846
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LOCUS AF044336 849 bp mRNA ROD 01-APR-1998
DEFINITION Mus musculus strain DBA/2N cyclin dependent kinase inhibitor p16INK4a (Cdkn2a) mRNA, complete cds.
ACCESSION AF044336
VERSION AF044336.1 GI:3002948
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 849)
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a) and p19(ARF), is a candidate for the plasmacytoma susceptibility locus, pctr1
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)
MEDLINE 98151529
REFERENCE 2 (bases 1 to 849)
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1998) NCI/NIH, 37 Convent Dr., Bethesda, MD 20892, USA
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BASE COUNT 187 a 217 c 273 g 172 t
ORIGIN
Query Match 75.0%; Score 640; DB 12; Length 849;
Best Local Similarity 98.5%; Pred. No. 1.7e-154;
Matches 646; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 196 GAATCCTGGACAGGTGATGATGGGCAAGTTCAGGTACAGCTCTTCTGCTCAACT 255
Db 194 GTACCCGATTCAGGTGATGATGGGCAAGTTCAGGTACAGCTCTTCTGCTCAACT 253


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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 507)
AUTHORS       Stone S., Jiang P. and Kamb, A.
TITLE         Mouse MTS1 gene
JOURNAL       Patent: US 5843756-A 44 01-DEC-1998;
FEATURES      Location/Qualifiers
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BASE COUNT    86 a 157 c 165 g 99 t
ORIGIN

Query Match      44.8%; Score 382.2; DB 5; Length 507;
Best Local Similarity 98.0%; Pred. No. 4.6e-88;
Matches 387; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 113 GTACCCGATTCAGGTGATGATGGGCAAGTTTCAGCTAGCAGCTCTTCTGTCTCAACT 172

Qy 256 ACGGTGCAGATTCGAACTCGAGGACCCCACTACCTTCTCCGCCGGTGCACGACGAG 315
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Db 173 ACGGTGCAGATTCGAACTCGAGGACCCCACTACCTTCTCCGCCGGTGCACGACGAG 232

Qy 316 CCGCGGAAGGCTTCCTGGACACGCTGGTGTGCTGCACGGGTTCAGGGGCTCGGCTGGATG 375
    |||||
Db 233 CCGCGGAAGGCTTCCTGGACACGCTGGTGTGCTGCACGGGTTCAGGGGCTCGGCTGGATG 292

Qy 376 TCGCGGATGCTGGGGTGCCTTCGCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACA 435
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Db 293 TCGCGGATGCTGGGGTGCCTTCGCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACA 352

Qy 436 TCGTGCATATTGCTTCCGCTGGTGTGCTCTTTGTTTCCGCTGGTGGTCTTTGTGTA 495
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Qy 496 CCGCTGGGAACGTCGCCACGACGCGGCATAGCTTCAGCTCAAGCACGCCGCCAGGGCCC 555
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Db 413 CCGCTGGGAACGTCGCCACGACGCGGCATAGCTTCAGCTCAAGCACGCCGCCAGGGCCC 472

Qy 556 TGGAACTTCGGCGGCAATCCCAAGACGAGACTAA 590
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Db 473 TGGAACTTCGGCGGCAATCCCAAGACGAGACTAA 507

RESULT 8
AR001335
LOCUS          AR001335      395 bp      DNA      PAT      04-DEC-1998
DEFINITION     Sequence 25 from patent US 5739027.
ACCESSION      AR001335
VERSION        AR001335.1 GI:3963402
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 395)
AUTHORS        Kamb, A.
TITLE          MTS1E1.beta. gene
JOURNAL        Patent: US 5739027-A 25 14-APR-1998;
FEATURES       Location/Qualifiers
               source
               1..395
BASE COUNT     73 a 109 c 128 g 85 t
ORIGIN

Query Match      44.0%; Score 375; DB 5; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.2e-86;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 75 AAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAGACAGCG-AGTGC 133
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Db 1 AAGAGAGGGTTTCTTGGTAAAGTTCTGTCGATCCCGAGACCCAGACAGCGTAGTGC 60

Qy 134 GCTCTGGCTTTCGTGAACATGTTCTTGAGGCTAGAGAGGATCTTTGAGAAGAGGCGCCGAC 193
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Db 61 GCTCTGGCTTTCGTGAACATGTTCTTGAGGCTAGAGAGGATCTTTGAGAAGAGGCGCCGAC 120

Qy 194 CGGAATCCTGGACCAAGGTGATGATGGGCAACGTTTCACGTAGCAGCTCTTCTGCTCAA 253
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Db 121 CGGAATCCTGGACCAAGGTGATGATGGGCAACGTTTCACGTAGCAGCTCTTCTGCTCAA 180

Qy 254 CTACGGTGCAGATTCGAACCTCGAGGACCCCACTACCTTCTCCGCCGGTGCACGAGCG 313
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Qy 314 AGCCGGGAAGGCTTCTTGGACACGCTGGTGTGCTGCACGGGTTCAGGGGTCGGCTGGA 373
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Db 241 AGCCGGGAAGGCTTCTTGGACACGCTGGTGTGCTGCACGGGTTCAGGGGTCGGCTGGA 300

Qy 374 TGTGCGGATGCCCTGGGTGCGCTTCCGCTGCGACTTGGCCCAAGAGCGGGGACATCAAGA 433
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Db 301 TGTGCGGATGCCCTGGGTGCGCTTCCGCTGCGACTTGGCCCAAGAGCGGGGACATCAAGA 360

Qy 434 CATCGTGGATATTGGTTCGCTCCGCTGGTGTCTTT 468
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Db 361 CATCGTGGATATTGGTTCGCTCCGCTGGTGTCTTT 395

RESULT 9
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LOCUS          AR037515      395 bp      DNA      PAT      29-SEP-1999
DEFINITION     Sequence 25 from patent US 5801236.
ACCESSION      AR037515
VERSION        AR037515.1 GI:5955371
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 395)
AUTHORS        Kamb, A.
TITLE          Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
JOURNAL        Patent: US 5801236-A 25 01-SEP-1998;
FEATURES       Location/Qualifiers
               source
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BASE COUNT     73 a 109 c 128 g 85 t
ORIGIN

Query Match      44.0%; Score 375; DB 5; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.2e-86;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 75 AAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGAGACCCAGACAGCG-AGTGC 133
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Qy 134 GCTCTGGCTTTCGTGAACATGTTCTTGAGGCTAGAGAGGATCTTTGAGAAGAGGCGCCGAC 193
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Db 61 GCTCTGGCTTTCGTGAACATGTTCTTGAGGCTAGAGAGGATCTTTGAGAAGAGGCGCCGAC 120

Qy 194 CGGAATCCTGGACCAAGGTGATGATGGGCAACGTTTCACGTAGCAGCTCTTCTGCTCAA 253
    |||||
Db 121 CGGAATCCTGGACCAAGGTGATGATGGGCAACGTTTCACGTAGCAGCTCTTCTGCTCAA 180

Qy 254 CTACGGTGCAGATTCGAACCTCGAGGACCCCACTACCTTCTCCGCCGGTGCACGAGCG 313
    |||||
Db 181 CTACGGTGCAGATTCGAACCTCGAGGACCCCACTACCTTCTCCGCCGGTGCACGAGCG 240

Qy 314 AGCCGGGAAGGCTTCTTGGACACGCTGGTGTGCTGCACGGGTTCAGGGGTCGGCTGGA 373
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.8e-78;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 CAGGTGATGATGGGCAACGTTACGTAGCAGCTTCTCTCACTACGTCGATG 266
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QY 267 TCGAACTCGAGGAGCCCACTACCTTCTCCCGCGGTGCACGACGCGCGGGAAGGC 326
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Db 161 TCGAACTCGAGGAGCCCACTACCTTCTCCCGCGGTGCACGACGCGCGGGAAGGC 220
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QY 327 TTCCTGGACACGCTGGTGTGTGTGACGCGGTGAGGGCTCGGCTGGATGTCGCGATGCC 386
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QY 387 TGGGGTCGCTGCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGGATAT 446
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Db 281 TGGGGTCGCTGCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGGATAT 340
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QY 447 TTGCGTTCGCTGGGTGCTTCTTGTGTTCCGCTGGGTGCTTTGTGTACCGCTGGGAAC 506
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Db 341 TTGCGTTCGCTGGGTGCTTCTTGTGTTCCGCTGGGTGCTTTGTGTACCGCTGGGAAC 400
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QY 507 GTGCCCCAGACGCGGGGATAGCTTCAGCTCAAGCACGCCCGCAGG 551
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Db 401 GTGCCCCAGACGCGGGGATAGCTTCAGCTCAAGCACGCCCGCAGG 445
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RESULT 13
LOCUS MSU79634 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus spretus cyclin-dependent kinase inhibitor protein (p16(INK4a))
ACCESSION U79634
VERSION U79634.1 GI:4098165
KEYWORDS western wild mouse.
SOURCE Mus spretus
ORGANISM Mus spretus
REFERENCE 1 (bases 1 to 339)
AUTHORS Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., and Fernandez-Piqueras J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., and Fernandez-Piqueras J.

TITLE Direct Submission
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid, Cantoblanco, Madrid, Madrid 28049, Spain
FEATURES
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ORIGIN

Query Match 39.7%; Score 339; DB 12; Length 339;
Best Local Similarity 100.0%; Pred. No. 6e-77;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 330 CTGACACGCTGGTGTGCTGCACGGGTGTCAGGCTCGGCTGGATGTCGCGATGCCCTGG 389
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Db 301 GCCCAGACCGGCGGATAGCTTCAGCTCAAGCACGCCCGC 339
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RESULT 14
LOCUS MMU79632 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
ACCESSION U79632
VERSION U79632.1 GI:4098151
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 339)
AUTHORS Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., and Fernandez-Piqueras J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences

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JOURNAL      in mouse inbred strains
REFERENCE     Unpublished
AUTHORS       Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
              Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE        Direct Submission
JOURNAL      Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
              Cantoblanco, Madrid, Madrid 28049, Spain
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Best Local Similarity 99.4%; Pred. No. 4e-76;
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QY 210 GTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCGATTCG 269
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QY 510 GCCCAGACCGACGGGATAGCTTCAGCTCAAGCACGCC 548
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Db 301 GCCCAGACCGACGGGATAGCTTCAGCTCAAGCACGCC 339

RESULT 15
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LOCUS      MMU79633 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (pl6(INK4a))
ACCESSION U79633
VERSION   U79633.1 GI:4098153
KEYWORDS  house mouse.
SOURCE    Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the pl6(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
Unpublished
2 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
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                TDGHSFSSSTP"
BASE COUNT   54 a 101 c 111 g 73 t
ORIGIN
Query Match  39.4%; Score 335.8; DB 12; Length 339;
Best Local Similarity 99.4%; Pred. No. 4e-76;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 210 GTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCGATTCG 269
      |||||
Db 1 GTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCGATTCG 60

QY 270 AACTGGAGAGACCCCACTACTCTTCCGCCGGTGCAGCGGCTCGGCTGGATGCGCGATTCG 329
      |||||
Db 61 AACTGGAGAGACCCCACTACTCTTCCGCCGGTGCAGCGGCTCGGCTGGATGCGCGATTCG 120

QY 330 CTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389
      |||||
Db 121 CTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 390 GGTCCGCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCATATTG 449
      |||||
Db 181 GGTCCGCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCATATTG 240

QY 450 CGTTCGCTGGGTGCTCTTTGCTTCCGCTGGGTGCTCTTTGCTACCCGTGGGAACGTC 509
      |||||
Db 241 CGTTCGCTGGGTGCTCTTTGCTTCCGCTGGGTGCTCTTTGCTACCCGTGGGAACGTC 300

QY 510 GCCCAGACCGACGGGATAGCTTCAGCTCAAGCACGCC 548
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Db 301 GCCCAGACCGACGGGATAGCTTCAGCTCAAGCACGCC 339

Search completed: July 21, 2000, 06:05:30
Job time: 14864 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 06:18:48 ; Search time 107.17 Seconds
(without alignments)
1991.358 Million cell updates/sec

Title: US-09-016-869A-5
Perfect score: 853
Sequence: 1 GGACTACAGCGCGGAGCA.....GATACCTTTTAAATGTCAA 853

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851.4	99.8	853	1 T02965	Cell-cycle regulat
2	674.4	79.1	713	1 T62485	Murine ARF-p19 CDN
3	382.2	44.8	507	1 V70623	Mouse multiple tum
4	375	44.0	395	1 V11259	Mouse p16 CDNA fra
5	375	44.0	395	1 V53840	Nucleotide sequenc
6	375	44.0	395	1 V70604	CDNA encoding a mu
7	226	26.5	1131	1 V70594	CDNA encoding a hu
8	224.4	26.3	1131	1 T00744	Multiple tumour su
9	224.4	26.3	1131	1 Q99164	Human MRS polypept
10	224.4	26.3	1131	1 T69780	Human multiple tum
11	224.4	26.3	1131	1 V11249	Human MTS1-beta
12	224.4	26.3	1131	1 V53830	Coding sequence 1
13	208.6	24.5	540	1 T62486	Human ARF-p19 CDNA
14	162.4	19.0	393	1 V70624	Mouse multiple tum
15	159.2	18.7	447	1 T00736	Multiple tumour su
16	159.2	18.7	447	1 Q99158	Human multiple tum
17	159.2	18.7	471	1 V11238	Human MTS1 CDNA. D
18	159.2	18.7	471	1 V53819	Nucleotide sequenc
19	159.2	18.7	471	1 V70583	CDNA encoding a hu
20	159.2	18.7	737	1 X26233	Truncated p27/p16
21	159.2	18.7	782	1 X26234	Truncated p27/p16
22	159.2	18.7	947	1 T00747	Multiple tumour su
23	159.2	18.7	947	1 T72311	Human multiple tum
24	159.2	18.7	947	1 V11270	Human MTS1 CDNA va
25	159.2	18.7	947	1 V53851	Coding sequence 3
26	159.2	18.7	947	1 V70615	CDNA encoding a hu
27	159.2	18.7	948	1 Q63491	Inhibitor of cyclin
28	159.2	18.7	987	1 T60951	Tumour suppressor
29	159.2	18.7	994	1 T02962	Cell-cycle regulat
30	159.2	18.7	1028	1 X26231	Truncated p27/p16
31	159.2	18.7	1073	1 X26232	Truncated p27/p16
32	159.2	18.7	1098	1 T74053	CDK inhibitory fus
33	159.2	18.7	1098	1 X26224	Human p16p27 fusio

ALIGNMENTS

RESULT 1
T02965
ID T02965 standard; cDNA; 853 BP.
AC T02965;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p13.5 CDNA.
KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;
KW ss; ds.
OS Mus sp.
FH Key
FT cds
FT W09528483-A1.
FN 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach OH, Demetrick DJ, Hannon GJ, Serrano M;
DR WPI: 95-373798/48.
DR P-PSDB: R85120.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
PT and related nucleic acids, antibodies etc., used in diagnosis and
PT therapy of abnormal cell proliferation, degeneration etc.
PS Example 4; Page 80; 109pp; English.
CC cDNA (T02965) coding for the mouse cell-cycle regulatory (CCR)
CC protein p13.5 (R85120) was isolated from an embryonal stem cell
CC library using a probe based on human CCR p16 CDNA (T02962).
CC The isolated cDNA can be used: to detect mutations in CCR
CC genes that lead to cell proliferation; to breed transgenic
CC animals to study cellular disorders involving CCR allele
CC mutation/misexpression; and to correct CCR-deficient cells
CC (gene therapy).
SQ Sequence 853 BP; 192 A; 207 C; 274 G; 180 T;
Query Match 99.8%; Score 851.4; DB 1; Length 853;
Best Local Similarity 99.9%; Pred. No. 2.1e-234;
Matches 852; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAGTACAGCAGCGGAGCATGGTTCGTCAGTGTCTTCTTGGTGAAGTTCGCGGAGCCAG 120
Db 1 GGAGTACAGCAGCGGAGCATGGTTCGTCAGTGTCTTCTTGGTGAAGTTCGCGGAGCCAG 120
QY 61 GGCGCCGCCACACCCAGAGAGGGTTTCTTGGTGAAGTTCGTCAGTGTCTTGGTGAAGTTCGCGGAGCCAG 120
Db 61 GGCGCCGCCACACCCAGAGAGGGTTTCTTGGTGAAGTTCGTCAGTGTCTTGGTGAAGTTCGCGGAGCCAG 120
QY 121 GACAGCGAGCTGGGCTCTGGCTTTCGTTGACATGTGTTGGAGCTAGAGAGGATCTTGAG 180
Db 121 GACAGCGAGCTGGGCTCTGGCTTTCGTTGACATGTGTTGGAGCTAGAGAGGATCTTGAG 180
QY 181 AAGAGGGCGCCACCCGGAATCTCTGGACCATGGTGTATGATGTGGCAACGTTTCACGTAGCAG 240


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Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 433
Db 301 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 360
QY 434 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 468
Db 361 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 395

RESULT 5
V53840
ID V53840 standard; DNA; 395 BP.
AC V53840;
DT 04-DEC-1998 (first entry)
DE Nucleotide sequence of nucleic acid 6.
KW Multiple tumour suppressor; MTS1B1S; human; cancer; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
PN US5801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-U03316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-494842/42.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure; Column 83-84; 73pp; English.
CC This is the nucleotide sequence of a nucleic acid used in the
CC method of the invention involving the use of the multiple tumour
CC suppressor (MTS) gene to diagnose and treat human cancers. The MTS
CC gene is useful in the diagnosis and prognosis of human cancer, e.g.
CC by standard nucleic hybridisation techniques, of patient samples.
CC The mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

Query Match 44.0%; Score 375; DB 1; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.7e-98;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACAGCG-AGCTGC 133
Db 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACAGCGTAGCTGC 60
QY 134 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 193
Db 61 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 120
QY 194 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCG-AGCTGC 313
Db 181 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCGTAGCTGC 240
QY 314 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 193
Db 61 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 120
QY 194 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCG-AGCTGC 313
Db 181 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCGTAGCTGC 240
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QY 314 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 373
Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 433
Db 301 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 360
QY 434 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 468
Db 361 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 395

RESULT 6
V70604
ID V70604 standard; cDNA; 395 BP.
AC V70604;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a murine multiple tumour suppressor lEl-beta protein.
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Mus sp.
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI; 99-044585/04.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 8; Fig 14; 80pp; English.
CC The present sequence encodes murine multiple tumour suppressor lEl-beta
CC (MTS1El-beta) protein. Primers designed from the gene can be used to
CC design primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

Query Match 44.0%; Score 375; DB 1; Length 395;
Best Local Similarity 98.5%; Pred. No. 3.7e-98;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACAGCG-AGCTGC 133
Db 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACAGCGTAGCTGC 60
QY 134 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 193
Db 61 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 120
QY 194 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 253
Db 121 CGGAATCTGGACAGGTGATGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCG-AGCTGC 313
Db 181 CTACGGTGCAGATTCGAATTCGTCGATCCCGGAGACCCAGGACAGCGTAGCTGC 240
QY 314 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 373
Db 241 AGCGCGGAGGCTTCCTGGACACGCTGGTGGTGTGCTGCACGGGTACAGGGGCTCGGCTGGA 300
QY 374 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 433
Db 301 TGTGGCGATGCTCGGGTGGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 360
QY 434 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 468
Db 361 CATCGTGGGATATTTGGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 395
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RESULT 7
V70594
ID V70594 standard; cDNA; 1131 BP.
AC V70594;
DE 03-FEB-1999 (first entry)
KW Multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 338..655
FT /tag= a
FT /product= MTS1E1-beta
FT
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR WPI: 99-044585/04.
DR P-PSDB; W80525.
PT Mouse multiple tumour suppressor gene segment - useful for primer design
PS Example 8; Fig 12A-B; 80pp; English.
CC The present sequence encodes a human multiple tumour suppressor 1E1-beta (MTS1E1-beta) protein. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
CC
SQ Sequence 1131 BP; 231 A; 327 C; 344 G; 229 T;

Query Match 26.5%; Score 226; DB 1; Length 1131;
Best Local Similarity 69.9%; Pred. No. 2.7e-55;
Matches 320; Conservative 0; Mismatches 135; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGGCGCC 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 CGCGCGAGAACATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGGCG 190

QY 69 CACTCAAGAGAGGTTTCTTGGTGAAGTTCTGTCAGTTCAGGATTACGCGCGGCGCC 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 CGCGCGAGTGGGTTTCTGTTGTTCACTCCCGGGCTCAGCGGGGAGTGGCGAGC 250

QY 129 GCTGCGCTCTGGCTTTCTGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAAGAGG 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 CAGGGGCGCGCGGCTGTGGCCCTGCTGCTGATGCTACTGAGGAGCCAGCGTCTAG 310

QY 189 CGCACCGGAATCCT---GGACCAAGTGTATGATGATGGCAACGTTACGTAGGAGCT 245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGCAGCGGTTCTTAGAAGACCAAGTGTATGATGGGAGCGCGGAGTGGGAGCTG 370

QY 246 CTGCTCAACTACGGTTCAGATTGGAATCGAGAGACCCCACTACCTTCTCCCGCGG 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 CTGCTCTCCAGCGCGGAGCCCACTAGCGGAGCCCGGAGCTCTACCCACCGCTG 430

QY 306 CAGCAGCGAGCGCGGAGGCTTCTTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 CAGCAGCTGCGCGGAGGCTTCTTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 490

QY 366 CGGCTGATGTCGCGATGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 CGGCTGATGTCGCGATGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 550

QY 426 CATCAAGACATGTCGATATTTGCGTTCCGCTGGGTG 463
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 551 CATCGGATGTCGCGAGTACCTGCGCGGCTGCGG 588

RESULT 8
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T00744
ID T00744 standard; cDNA; 1131 BP.
AC T00744;
DE 08-MAY-1996 (first entry)
KW Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) gene ORF.
KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 338..655
FT /tag= a
FT
PN W09525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI: 95-344626/44.
DR P-PSDB; R81700.
PT Detecting polymorphism associated with cancer pre-disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening
PS Example 7; Pages 100-101; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
CC
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGGCGCC 68
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 CGCGCGAGAACATGGTTCGCAGGTTCTTGGTCACTGTAGGATTACGCGCGGCG 190

QY 69 CACTCAAGAGAGGTTTCTTGGTGAAGTTCTGTCAGTTCAGGATTACGCGCGGCGCC 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 CGCGCGAGTGGGTTTCTGTTGTTCACTCCCGGGCTCAGCGGGGAGTGGCGAGC 250

QY 129 GCTGCGCTCTGGCTTTCTGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAAGAGG 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 251 CAGGGGCGCGCGGCTGTGGCCCTGCTGCTGATGCTACTGAGGAGCCAGCGTCTAG 310

QY 189 CGCACCGGAATCCT---GGACCAAGTGTATGATGATGGCAACGTTACGTAGGAGCT 245
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 311 AGCAGCGGTTCTTAGAAGACCAAGTGTATGATGGGAGCGCGGAGTGGGAGCTG 370

QY 246 CTGCTCAACTACGGTTCAGATTGGAATCGAGAGACCCCACTACCTTCTCCCGCGG 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 CTGCTCTCCAGCGCGGAGCCCACTAGCGGAGCCCGGAGCTCTACCCACCGCTG 430

QY 306 CAGCAGCGAGCGCGGAGGCTTCTTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 431 CAGCAGCTGCGCGGAGGCTTCTTGGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 490

QY 366 CGGCTGATGTCGCGATGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 CGGCTGATGTCGCGATGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 550

QY 426 CATCAAGACATGTCGATATTTGCGTTCCGCTGGGTG 463
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 551 CATCGGATGTCGCGAGTACCTGCGCGGCTGCGG 588
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RESULT 9
Q99164
ID Q99164 standard; cDNA; 1131 BP.
AC Q99164;
DT 03-MAY-1996 (first entry)
DE Human MTS polypeptide, MTS1E1-beta encoding cDNA.
KW Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
OS gene therapy; chronic; ds.
FH Homo sapiens.
FH Key Location/Qualifiers
FT cds 338..655
FT /tag= a
FT /product= MTS1E1-beta
PD WO9525429-A1.
PN 28-SEP-1995.
PD 17-MAR-1995; U03316.
PF 18-MAR-1994; US-214581.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215088.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR (MYRI-) MYRIAD GENETICS INC.
PA Kamb A;
PI P-PSDB; R80947.
DR WPI; 95-344401/44.
DR P-PSDB; R80947.
PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
PT melanoma or leukaemia
PS Claim 4; Page 100-101; 156pp; English.
CC The cDNA sequences encoding several multiple tumour suppressor (MTS)
CC polypeptides have been isolated and sequenced. This sequence encodes
CC the MTS polypeptide MTS1E1-beta (R80947). MTS polypeptide-encoding cDNAs
CC and mutants of these are useful for the diagnosis or prognosis of
CC human cancer. Germ-line mutations of MTS cDNAs can be used for
CC diagnosing predisposition to melanoma, leukaemia, astrocytoma,
CC glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers
CC of the pancreas, thyroid, ovary, uterus, kidney, stomach and
CC rectum. The wild-type gene is useful for gene therapy and MTS
CC polypeptides may also be used for protein replacement therapy. Also
CC the polypeptides or cells contg. an altered MTS gene are useful for
CC screening for potential cancer therapeutics.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGGCGGCC 68
DB 131 GCGCGGAGAACATGGTGCAGGTTTCATGGTACCTCCGGATTCGGCGCGGTCCGAC 190
QY 69 CACTCCAAAGAGAGGTTTCTTGGTGAAGTTGTCGATCCCGGAGACCCAGGACGCGA 128
DB 191 GCGCGGAGTGAAGTTTCTGTTTCATATCCCGCGGTACACGGGGGAGTGGGCGAC 250
QY 129 GCTGGCTCTGGCTTCGTGAACATGTTGTTGAGCTAGAGAGGATCTTGAGAGAGGGC 188
DB 251 CAGGGGCGCGCGCGCTGTGGCCCTCGTGTGATCTACTGAGGAGCCAGCGTCTAGGGC 310
QY 189 GCGACCGGAATCCT---GGACCAAGTGTATGATGGCAACGTTACGTAGCAGCTCTT 245
DB 311 AGCAGCCGCTTCTTAGAGACCAAGTGTATGATGGCAGCCGCGGAGTGGGAGCTG 370
QY 246 CTGCTCAACTAGGTGAGATTCGAATTCGAGGAGACCCCACTACCTTCTCCGCGCGGTG 305
DB 371 CTGCTGCTCCACGGCGGAGGCCCAACTGCGCGGAGCCCGGCACTCTCACCGGACCGGTG 430
QY 306 CACGACGACGCGCGGGAAGGCTTCTTGGACACGCTGGTGGTCTGCACGGGTACGGGCT 365

RESULT 10
T69780
ID T69780 standard; cDNA; 1131 BP.
AC T69780;
DT 10-SEP-1997 (first entry)
DE Human multiple tumour suppressor gene 1 Elbeta.
KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
KW Elbeta; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 338..655
FT /tag= a
FT US5624819-A.
PN 29-APR-1997.
PD 18-MAR-1994; 214582.
PF 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003537.
PR 07-JUN-1995; US-474177.
PA (MYRI-) MYRIAD GENETICS INC.
PI (UTAH) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 97-258217/23.
DR P-PSDB; W19254.
DR Human mutant multiple tumour suppressor gene sequences - for
PT production of recombinant mutant polypeptide(s)
PS Disclosure; Columns 73-74; 72pp; English.
CC The present sequence the human multiple tumour suppressor gene 1
CC (MTS1) Elbeta, useful in cancer diagnosis.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
```

Db 431 CAGGAGCTGCCGGAGGGCTCTCTGGACACGCTGGTGGTGCACCGCGCGGGCG 490
QY 366 CGGCTGGATGTGGCGATGCCCTGGGGTGCCTGCGCTCGACTGGCCCAAGAGCGGGGA 425
Db 491 CGGCTGGAGTGGCGATGCCCTGGGGCGCTCTGCCGCTGGACTGGCTGAGGAGCTGGGC 550
QY 426 CATCAAGACATCGTGGGATATTGGCTTCGGCTGGGTG 463
Db 551 CATCGGATGTCGACGGTACCTGCGCGGGCTGGCGG 588

RESULT 11
V11249
ID V11249 standard; cDNA; 1131 BP.
AC V11249;
DT 15-JUL-1998 (first entry)
DE Human MTS1E1-beta cDNA.
KW MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
KW germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
OS Homo sapiens.
FH Key
FT CDS

Location/Qualifiers
338..655
/*tag= a
/product= MTS1E1-beta
/note= "multiple tumour suppressor"

US5739027-A.
PN 14-APR-1998.
PD P-PSDB; W40525.
PF 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-250421/22.
DR P-PSDB; W40525.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PS Claim 1; Fig 12; 72pp; English.
CC This cDNA sequence encodes a human multiple tumour suppression protein,
CC MTS1E1-beta. The MTS gene locus is also referred to as the familial
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTTCGAGGTTCTTGGTCACTCTAAGATTACGCGCGCGCGCC 68
Db 131 CGCGCAGACATGGTTCGAGGTTCTTGGTCACTCTAAGATTACGCGCGCGCGCC 190
QY 69 CACTCAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAGACGCGA 128
Db 191 CGCGCGAGTGGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGTGGCGAGCAC 250
QY 129 GCTGCGCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTCAGAGAGGCG 188
Db 251 CAGGGGCGCGCGCTGTGGTCTGCTGATGCTACTGAGGAGCCACGCTCTAGGGC 310
QY 189 CGCACCAGGAATCTCT--GGACCAAGTGTATGATGATGGCAACGTTTCACGTFAGCAGCTCT 245
Db 311 AGCAGCGGCTTCTTAGAAGACCAAGGTCATGATGATGGCAGCCCGCGAGTGGCGGAGCTG 370

QY 246 CTGCTCAACTAGGTGCAGATTCTGAACCTGCGAGGACCCCACTACCTTCTCCCGCGCGGTG 305
Db 371 CTGCTGCTCCACGGCGGAGAGCCCAACTGCGCGGACCCCGCACTCTCACCGCAGCCGCTG 430
QY 306 CACGACGAGCGCGGAGAGGCTTCTGACACGCTGGTGGTCTGACGGGTTCAGGGGCT 365
Db 431 CACGACGCTGCCGCGGAGGGCTTCTGACACGCTGGTGGTCTGACCGCGCGCGGGGGG 490
QY 366 CGGCTGGATGTGCGCGATGCTGCGGTGCGCTGCGCTGCGCTGCGCTGCGCTGCGGTG 425
Db 491 CGGCTGGACGTGCGCGATGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 550
QY 426 CATCAAGACATCGTGGGATATTGGCTTCGGCTGGGTG 463
Db 551 CATCGGATGTCGACGGTACCTGCGCGGGCTGGCGG 588

RESULT 12
V53830
ID V53830 standard; cDNA; 1131 BP.
AC V53830;
DT 04-DEC-1998 (first entry)
DE Coding sequence 1 of the multiple tumour suppressor MTS1E1S.
KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
FH Key
FT CDS

Location/Qualifiers
338..655
/*tag= a
/product= "human MTS1E1S"

US5801236-A.
PN 01-SEP-1998.
PD 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI; 98-494842/42.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Example 7; Column 73-76; 73pp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor
CC (MTS1E1S) gene, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;

Query Match 26.3%; Score 224.4; DB 1; Length 1131;
Best Local Similarity 69.7%; Pred. No. 7.8e-55;
Matches 319; Conservative 0; Mismatches 136; Indels 3; Gaps 1;

QY 9 GCAGCGGAGCATGGTTCGAGGTTCTTGGTCACTCTAAGATTACGCGCGCGCGCC 68
Db 131 CGCGCAGAACATGGTTCGAGGTTCTTGGTCACTCTAAGATTACGCGCGCGCGCC 190
QY 69 CACTCAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAGACGCGA 128

```
Db 191 GCGCGGAGTGGGTTTCTGGTTTACATCCGCGGCTCAGGGGAGTGGCAGCAC 250
Qy 129 GCTGGCTCTGGCTTCTGTAACATGTTGTAGGCTAGAGAGATCTTGAAGAAGGGC 188
Db 251 CAGGGGCGCGCGCTGTGGCCCTCTGCTGATGCTACTGAGAGCCACGCTTAGGGC 310
Qy 189 GGCACCGGAATCCT---GGACCAAGTGATGATGATGGCAACGTTACGTTAGAGCTCTT 245
Db 311 AGCAGCGCTTCTCTAGAAGACCAAGTCTATGATGATGGCAGCGCCGAGTGGCGAGCTG 370
Qy 246 CTGCTCACTACGTGTCAGATTCGAATCTGGAGGACCCCACTACCTCTCTCCCGCGGGT 305
Db 371 CTGCTGTCCACGCGCGGAGCCCACTGCGCGACCCCGCCCACTCTCACCCACCGCTG 430
Qy 306 CACGACGCGCGCGGAGGCTTCTTGACACAGCTGTGTGTGTCACGGGTCAGGGGCT 365
Db 431 CACGACGCTGCGCGGAGGCTTCTTGACACAGCTGTGTGTGTCACGGGTCAGGGGCT 490
Qy 366 GCGCTGATGTCGCGGATGCTGGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 425
Db 491 CCGCTGAGCTGCGGATGCTGGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 550
Qy 426 CATCAAGACATCTGCGATATTTGCTTCCGCTGGGTG 463
Db 551 CATCGCATGTCGACAGGTAACCTGCGCGGCTGCGGG 588

RESULT 13
T62486
ID T62486 standard; cDNA; 540 BP.
AC T62486;
DT 16-AUG-1997 (first entry)
DE Human ARF-p19 cDNA.
KW ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis;
KW gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;
KW inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 142..540
FT FT /*tag= a
FT FT /product= ARF-p19
FT FT 338..538
FT FT /*tag= b
FT FT /product= INK4a-p16 C-terminal fragment
FT FT W09712060-A1.
FT FT 03-APR-1997.
FT FT 25-SEP-1996; U15312.
FT FT 27-SEP-1995; US-534975.
FT FT (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
FT FT Quelle DE, Sherr CJ;
FT FT WPI; 97-212919/19.
FT FT P-PSDB; W16323-24.
FT FT Nucleic acid encoding ARF-p19 which induces cell cycle arrest when
FT FT overexpressed - used for diagnosis and treatment of cancer, and for
FT FT drug screening
FT FT Claim 2; Fig 7; 49pp; English.
FT FT A human cDNA molecule (T62486) corresponds to INK4a beta
FT FT transcripts and includes a reading frame coding for a novel protein
FT FT (W16323). Designated ARF-p19, which induces cell cycle arrest when
FT FT overexpressed. This reading frame asymptotically overlaps a second
FT FT reading frame that encodes INK4a-p16 (C-terminal region given in
FT FT W16324), an inhibitor of the cyclin D-dependent kinases CDK4 and
FT FT CDK6. Economical reutilization of protein coding sequences in this
FT FT manner is without precedent in mammalian genomes and the unitary
FT FT inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement
FT FT for both proteins in cell cycle control. ARF-p19 nucleic acids can
FT FT be used as probes or primers, esp. for cancer diagnosis, or in gene
FT FT therapy protocols to induce cell arrest in eukaryotes or (antisense)
FT FT CC to inhibit ARF-p19 activity, and to create transgenic animals useful
FT FT CC as models for cancer.
FT FT Sequence 540 BP; 68 A; 173 C; 216 G; 83 T;
```

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Query Match 24.5%; Score 208.6; DB 1; Length 540;
Best Local Similarity 71.3%; Pred. No. 1.9e-50;
Matches 290; Conservative 0; Mismatches 114; Indels 3; Gaps 1;

Qy 9 GCAGCGGAGAGTGGGTCGAGGTTCTTGGTCACTGTAAGGATTCAGGCGCGGCGCGCC 68
Db 131 GCGGCGAGAACATGTCGTCAGGTTCTTGGTGACCTCCGATTCGGCGCGCTGCGGCC 190
Qy 69 CACTCCAAAGAGAGGTTTCTTGGTGAAGTTCGTCGATCCCGGAGACCCAGGACGGA 128
Db 191 CCGCCGAGTGAAGGTTTCTTGGTTCATCCCGCGCTCAGGGGAGTGGCAGCGC 250
Qy 129 GCTGCGCTCTGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAG 188
Db 251 CAGGGGCGCGCGCTGTCGCCCTCGTGTGCTGCTACTGAGGAGCCAGCTCTAGGGC 310
Qy 189 CGCACCGGAATCCT---GGACCAAGTGATGATGATGGCAACGTTACGTTAGAGCTCTT 245
Db 311 AGCAGCGCTTCTCTAGAAGACCAAGTCTATGATGATGGCAGCGCCGAGTGGCGAGCTG 370
Qy 246 CTGCTCAACTACGTGTCAGATTCGAATCTGGAGGACCCCACTACCTCTCTCCCGCGG 305
Db 371 CTGCTGTCTCCACGCGCGGAGCCCACTGCGCGACCCCGCCCACTCTCACCCGACCG 430
Qy 306 CACGACGCGCGCGGAGGCTTCTTGACACAGCTGTGTGTGCTGCGAGGCTCAGGGGCT 365
Db 431 CACGACGCTGCGCGGAGGCTTCTTGACACAGCTGTGTGTGCTGCGAGGCTGCGCGG 490
Qy 366 GCGCTGATGTCGCGGATGCTGGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 412
Db 491 CCGCTGAGCTGCGCGATGCTGGGTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 537

RESULT 14
W70624
ID W70624 standard; cDNA; 393 BP.
AC W70624;
DT 03-FEB-1999 (first entry)
DE Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence.
KW Murine; multiple tumour suppressor 2 gene; MTS2; cancer; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT cds 1..393
FT FT /*tag= a
FT FT 132..133
FT FT /*tag= b
FT FT /note= "splice site"
FT FT US5843756-A.
FT FT 01-DEC-1998.
FT FT 28-JUL-1995; 058735.
FT FT 28-JUL-1995; US-508735.
FT FT 07-JUN-1995; US-487033.
FT FT (MYRI-) MYRIAD GENETICS INC.
FT FT Jiang P, Kamb A, Stone S;
FT FT WPI; 99-044585/04.
FT FT P-PSDB; W70823.
FT FT Mouse multiple tumour suppressor gene segment - useful for primer
FT FT design
FT FT Example 7; Fig 18; 80pp; English.
FT FT The present sequence encodes mouse multiple tumour suppressor 2
FT FT (MTS2) gene. The MTS1 gene can be used to design primers to
FT FT detect abnormalities i.e. polymorphisms which may predispose
FT FT towards malignancies such as melanoma, leukaemia, astrocytoma,
FT FT lymphoma, glioma, as well as tumours of e.g. the breast,
FT FT thyroid, pancreas, uterus and kidneys.
FT FT Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;

Query Match 19.0%; Score 162.4; DB 1; Length 393;
Best Local Similarity 77.8%; Pred. No. 2.7e-37;
Matches 196; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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QY 206 CCAGGTGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCACTACGTCGAGC 265
Db 129 CCAGGTGATGATGGGCAACGTCAGAGTGTGCTGTCTTCCACGGAGCAGA 188
QY 266 TTGAACCTGCGAGGACCCCACTACCTTCTCCGCGCCGCTGCACGACGCGCGGAAGG 325
Db 189 ACCCAACTGCGCGACCCCTGCCACCCCTTACCAGACCTGTGCACGACGAGCTCGGGAAG 248
QY 326 CTTCTGAGACAGCTGTGTGCTGCACGGGTGAGGGCTCGGCTGGATGTCGCGGATGC 385
Db 249 CTTCTGAGACAGCTGTGTGCTGCACGGGTGAGGGCTCGGCTGGATGTCGCGGATGC 308
QY 386 CTGGGTCGCGCTCGGCTGCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCAGTA 445
Db 309 CTGGGTCGCGCTCGGCTGCGACTTGGCTGAAGAGCAGGCGCCACCGTGACATTCGAGGTA 368
QY 446 TTTGCGTTCCGC 457
Db 369 TCTGCACGCTGC 380

RESULT 15
T00736
ID T00736 standard; cDNA; 447 BP.
AC T00736;
DT 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 1 (MTS1) gene ORF.
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; open reading frame; ORF; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 1..447
FT /tag= a
PN WO9525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI; 95-344626/44.
DR P-PSDB; R81701.
DT Detecting polymorphism associated with cancer pre:disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Example 8; Pages 91-92; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1
CC gene ORF T00736 (which encodes R81701) mutant sequences T00749/50.
CC The above assay can also be used in the diagnosis and prognosis of
CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CC cancers, etc.
SQ Sequence 447 BP; 64 A; 147 C; 172 G; 64 T;
```

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Query Match 18.7%; Score 159.2; DB 1; Length 447;
Best Local Similarity 74.6%; Pred. No. 2.4e-36;
Matches 200; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
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QY 196 GAATCCTGACAGGTGATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACT 255
Db 113 GGAGGCCCATCCAGGTGATGATGGGCAACGTCGCGCGGAGCTGTGCTGCTCC 172
QY 256 ACGGTGACAGATTCGAACGCGGAGGACCCCACTACCTTCTCCGCGCGGTGCACGACGAG 315
Db 173 ACGGCGCGGAGCCCAACTGCGCGGACCCCGGCACTCTCACCGGACCCCGTGCACGACGCTG 232
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QY 316 CGCGGGAAGGCTTCTCTGACACACGCTGCTGGTGTGCACGCTCAGGGGCTCGGCTGGATG 375
Db 233 CCCGGGAGGGCTTCTCTGACACACGCTGCTGGTGTGCACGCGCGGGCGGGCTGGACG 292
QY 376 TGC CGGATGCTTGGGGTCTGCGCTGCGCTTGGCCCAAGAGCGGGGACATCAAGACA 435
Db 293 TGC CGGATGCTTGGGGTCTGCGCTGCGCTTGGCCCAAGAGCGGGGACATCGCGATG 352
QY 436 TCGTCCGATATTTTCGCTTCCGCTGGGTG 463
Db 353 TCGCACGGTACCTGCGCGGGCTCGGG 380
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Search completed: July 21, 2000, 06:18:54
Job time: 13651 sec

Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTACAGCGGGAGCATGGTGCAGGTTCTTGTCTACTGTAAAGATTACGCGGC 60
DB 1 GGAGTACAGCGGGAGCATGGTGCAGGTTCTTGTCTACTGTAAAGATTACGCGGC 60

QY 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCGTGGATCCCGGAGACCCAG 120
DB 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCGTGGATCCCGGAGACCCAG 120

QY 121 GACAGCGAGCTCGCTCTGGTCTTCTGTAACATGTGTGAGGCTAGAGAGATCTTGAG 180
DB 121 GACAGCGAGCTCGCTCTGGTCTTCTGTAACATGTGTGAGGCTAGAGAGATCTTGAG 180

QY 181 AAGAGGGCCGACCGGAATCTTGACCAAGTGTGATGGGCAAGTTCACGTAGCAG 240
DB 181 AAGAGGGCCGACCGGAATCTTGACCAAGTGTGATGGGCAAGTTCACGTAGCAG 240

QY 241 CTCCTCTCTCAACTACGGTGCAGATTCGAATCGGAGGAGCCCACTACCTTCTCCGCC 300
DB 241 CTCCTCTCTCAACTACGGTGCAGATTCGAATCGGAGGAGCCCACTACCTTCTCCGCC 300

QY 301 CGGTCCAGCAGCAGCGGGGAAAGGCTTCTGGACACGCTGGTGGTGTGACAGGGTTCAG 360
DB 301 CGGTCCAGCAGCAGCGGGGAAAGGCTTCTGGACACGCTGGTGGTGTGACAGGGTTCAG 360

QY 361 GGGCTCGGCTGGATGTGCGCGATGCTGGGTGCGCTGCCCTCGACTTGGCCCAAGAGC 420
DB 361 GGGCTCGGCTGGATGTGCGCGATGCTGGGTGCGCTGCCCTCGACTTGGCCCAAGAGC 420

QY 421 GGGGACATCAAGACATCGTGGATATTTGCGTTCGGTGGTGTCTTTGTGTTCCGCTG 480
DB 421 GGGGACATCAAGACATCGTGGATATTTGCGTTCGGTGGTGTCTTTGTGTTCCGCTG 480

QY 481 GGTGTCTTTGTGTACCTGGGACGTCGCCAGACGCGGAGCATAGCTTCAGCTCAA 540
DB 481 GGTGTCTTTGTGTACCTGGGACGTCGCCAGACGCGGAGCATAGCTTCAGCTCAA 540

QY 541 GCACGCCAGGCGGCTGGAATCTCGCGGCAATCCCAAGAGCAGAGCTAAATCGCGCTCA 600
DB 541 GCACGCCAGGCGGCTGGAATCTCGCGGCAATCCCAAGAGCAGAGCTAAATCGCGCTCA 600

QY 601 GCCCGCTTTTCTTCTAGTCTTCTAGCTTCTAGCTGATGCTAGCTGCTAGCTGCTG 660
DB 601 GCCCGCTTTTCTTCTAGTCTTCTAGCTTCTAGCTGATGCTAGCTGCTAGCTGCTG 660

QY 661 TAAAAATACATAATAATGCTTTTTCGAATCAGGAGGAGGAGGAGGAGGAGCAG 720
DB 661 TAAAAATACATAATAATGCTTTTTCGAATCAGGAGGAGGAGGAGGAGGAGGAGCAG 720

QY 721 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 721 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780

QY 781 GAAGCGCGCCGGAAGGAATAATGGCTGGATTTTAAAAAATAAATAAAGATACTT 840
DB 781 GAAGCGCGCCGGAAGGAATAATGGCTGGATTTTAAAAAATAAATAAAGATACTT 840

QY 841 TTTAAATGTCAA 853
DB 841 TTTAAATGTCAA 853

RESULT 2

US-08-893-274-5
; Sequence 5, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,

TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 213..587
US-08-893-274-5

Query Match 100.0%; Score 853; DB 4; Length 853;
Best Local Similarity 100.0%; Pred. No. 2.1e-239;
Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTACAGCGGGAGCATGGTGCAGGTTCTTGTCTACTGTAAAGATTACGCGGC 60
DB 1 GGAGTACAGCGGGAGCATGGTGCAGGTTCTTGTCTACTGTAAAGATTACGCGGC 60

QY 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCGTGGATCCCGGAGACCCAG 120
DB 61 GGGCGCCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCGTGGATCCCGGAGACCCAG 120

QY 121 GACAGCGAGCTCGCTCTGGCTTTTCGTGAACATGTGTGAGGCTAGAGAGATCTTGAG 180
DB 121 GACAGCGAGCTCGCTCTGGCTTTTCGTGAACATGTGTGAGGCTAGAGAGATCTTGAG 180

QY 181 AAGAGGGCCGACCGGAATCTTGACCAAGTGTGATGGGCAAGTTCACGTAGCAG 240

181 AGAGGGCCGACCGGAATCCTGGACAGGTGATGATGGCAACGTTACGTAGCAG 240
241 CTCCTTCTGCTCAACTACGGTGCAGATTGAACTCGCAGGACCCCACTACCTTCTCCCGCC 300
241 CTCCTTCTGCTCAACTACGGTGCAGATTGAACTCGCAGGACCCCACTACCTTCTCCCGCC 300
301 CGGTGCACGACGAGCGCGGGAAGGCTTCTTGACACCGTGGTGGTGCACGGGTCTAG 360
301 CGGTGCACGACGAGCGCGGGAAGGCTTCTTGACACCGTGGTGGTGCACGGGTCTAG 360
361 GSGCTCGGCTGGATGTCGCGATGCTGGGTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 420
361 GSGCTCGGCTGGATGTCGCGATGCTGGGTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 420
421 GGGACATCAAGACATCGTGGGATTTTGGCTTCCGCTGGGTCCTTGTGTGTTCCGCTG 480
421 GGGACATCAAGACATCGTGGGATTTTGGCTTCCGCTGGGTCCTTGTGTGTTCCGCTG 480
481 GGTGGTCTTTGTACCGCTGGGAACGTGCGCCAGACCCGACGGGCATAGCTTCAGCTCAA 540
481 GGTGGTCTTTGTACCGCTGGGAACGTGCGCCAGACCCGACGGGCATAGCTTCAGCTCAA 540
541 GCACGCCAGGCGCCCTGGAACTTCGGGGCAATCCCAAGACAGAGCTAAATCCGCTCA 600
541 GCACGCCAGGCGCCCTGGAACTTCGGGGCAATCCCAAGACAGAGCTAAATCCGCTCA 600
601 GCGCGCTTTTCTTCTTACCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATG 660
601 GCGCGCTTTTCTTCTTACCTTCTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATG 660
661 TAAATAACATAAATGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
661 TAAATAACATAAATGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
721 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
721 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
781 GAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
781 GAAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
841 TTTAAATGCTCAA 853
841 TTTAAATGCTCAA 853

RESULT 3
US-08-581-918A-5
Sequence 5, Application US/08591918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Elliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 213..587
US-08-581-918A-5

Query Match 100.0%; Score 853; DB 5; Length 853;
Best Local Similarity 100.0%; Pred. No. 2.le-239;
Matches 853; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGTACAGCAGCGGAGCATGGTGCAGAGTTCTTGGTCACTGTAAAGATTTCAGCGCGC 60
Db 1 GGAGTACAGCAGCGGAGCATGGTGCAGAGTTCTTGGTCACTGTAAAGATTTCAGCGCGC 60
QY 61 GGGCGCCCGCCACTCCAAAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAG 120
Db 61 GGGCGCCCGCCACTCCAAAGAGAGAGGTTTCTTGGTGAAGTTCTGTCGATCCCGGAGACCCAG 120
QY 121 GACAGGAGCTCGGCTCTCGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 180
Db 121 GACAGGAGCTCGGCTCTCGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG 180
QY 181 AAGAGGGCGCAGCGGAAATCCTGGACAGGTGATGATGGCAACGTTACGTAGCAG 240
Db 181 AAGAGGGCGCAGCGGAAATCCTGGACAGGTGATGATGGCAACGTTACGTAGCAG 240
QY 241 CTCCTTCTGCTCAACTACGGTGCAGATTTCGAACTTCGAGGACCCCACTACCTTCTCCCGCC 300
Db 241 CTCCTTCTGCTCAACTACGGTGCAGATTTCGAACTTCGAGGACCCCACTACCTTCTCCCGCC 300
QY 301 CGGTGCACGACGAGCGCGGGAAGGCTTCTTGACACCGTGGTGGTGCACGGGTCTAG 360
Db 301 CGGTGCACGACGAGCGCGGGAAGGCTTCTTGACACCGTGGTGGTGCACGGGTCTAG 360
QY 361 GGGCTCGGCTGGATGTCGCGATGCTGGGTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 420

Db	361	GGGCTGGGCTGGATGTGCGGATGCTCTGGGGTCCGCTGCCGCTCGACTTGGCCCAAGAC	420
Qy	421	GGGACATCAAGACATCGTCGGATATTTGGGTTCCGCTGGGTGCTCTTTGTGTTCGGCTG	480
Db	421	GGGACATCAAGACATCGTCGGATATTTGGGTTCCGCTGGGTGCTCTTTGTGTTCGGCTG	480
Qy	481	GGTGGTCTTTGTGTACCGCTGGGAAGCTCGCCAGACCCGACGGGCATAGCTTCAGCTCAA	540
Db	481	GGTGGTCTTTGTGTACCGCTGGGAAGCTCGCCAGACCCGACGGGCATAGCTTCAGCTCAA	540
Qy	541	GCAGGCCAGGGCCCTGGAACTTCGGGGCCAAATCCCAAGACAGAGCTAAATCCGGCTCA	600
Db	541	GCAGGCCAGGGCCCTGGAACTTCGGGGCCAAATCCCAAGACAGAGCTAAATCCGGCTCA	600
Qy	601	GCCGCGCTTTTCTCTTAGCTTCACCTTCAGCGATGCTAGCGTGCTAGCATGTGGCTT	660
Db	601	GCCGCGCTTTTCTCTTAGCTTCACCTTCAGCGATGCTAGCGTGCTAGCATGTGGCTT	660
Qy	661	TAAAAATACATATAATGCTTTTTTTGCAATCAGCGGGAGCAGAGAGGGAGGACAG	720
Db	661	TAAAAATACATATAATGCTTTTTTTGCAATCAGCGGGAGCAGAGAGGGAGGACAG	720
Qy	721	AAGGAGGAGGGAGGGAGGAGGAGCTGCACAGGAAGGAATGGCATGGAACCTGACC	780
Db	721	AAGGAGGAGGGAGGGAGGAGGAGCTGCACAGGAAGGAATGGCATGGAACCTGACC	780
Qy	781	GAAGGCGGCCCGGAAGGGAAATAATGGCTGGATTGTTTAAAAAAATAAAAAATAGATAC	840
Db	781	GAAGGCGGCCCGGAAGGGAAATAATGGCTGGATTGTTTAAAAAAATAAAAAATAGATAC	840
Qy	841	TTTAAATATGTCAA	853
Db	841	TTTAAATATGTCAA	853

RESULT

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PCT-US95-04636-5
; Sequence 5, Application PC//US9504636
; GENERAL INFORMATION:
;
; APPLICATION:
; TITLE OF INVENTION: Cell-Cycle Regul
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

```

Patent No. 5723313
GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Quelle, Dawn, E.
TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell
TITLE OF INVENTION: Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 28-SEP-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0590000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..548
FEATURE:
NAME/KEY: CDS
LOCATION: 43..551
US-08-534-975-1

Query Match 78.9%; Score 672.8; DB 2; Length 713;
Best Local Similarity 99.6%; Pred. No. 6.2e-187;
Matches 685; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGAGTACAGCAGCGGAGCATGGGTGCGCAGGTTCTTGGTCACTGTAAAGATTACAGCGCG 60
DB 24 GGAGTACAGCAGCGGAGCATGGGTGCGCAGGTTCTTGGTCACTGTAAAGATTACAGCGCG 83
QY 61 GGGCGCCCACTCAAGAGAGGTTTCTTGGTGAAGTCTGTCGGATCCGCGAGACCCAG 120
DB 84 GGGCGCCCACTCAAGAGAGGTTTCTTGGTGAAGTCTGTCGGATCCGCGAGACCCAG 143
QY 121 GACAGGCGAGCTGCGCTCTGCTTTCGTGAACATGTTGTCAGGCTAGAGAGGATCTTGAG 180
DB 144 GACAGGCGAGCTGCGCTCTGCTTTCGTGAACATGTTGTCAGGCTAGAGAGGATCTTGAG 203
QY 181 AAGAGGCGCCACCGGAATCCTGGACAGGTGATGATGATGGCAACGTTTCAGCTAGCAG 240
DB 204 AAGAGGCGCCACCGGAATCCTGGACAGGTGATGATGATGGCAACGTTTCAGCTAGCAG 263
QY 241 CTCTTCTGCTCACTAGGTCGAGATTCGAACCTCGGAGGACCCACTACCTTCTCCGCC 300
DB 264 CTCTTCTGCTCACTAGGTCGAGATTCGAACCTCGGAGGACCCACTACCTTCTCCGCC 323
QY 301 CGGTGACGACGACGCGCGGAAGGCTTCTGGACAGCTGGTGGTCTGCTGACGGGTGAG 360
DB 324 CGGTGACGACGACGCGCGGAAGGCTTCTGGACAGCTGGTGGTCTGCTGACGGGTGAG 383

QY 361 GGGCTCGGCTGGATGTGCCGATGCTGGGTGCGGCTGCCGCTCGACTTGGGCCAAGAGC 420
DB 384 GGGCTCGGCTGGATGTGCCGATGCTGGGTGCGGCTGCCGCTCGACTTGGGCCAAGAGC 443
QY 421 GGGGACATCAAGACATCGTGGCCATATTTCCGTTCCGCTGGTGGTCTTGTGTTCCGCTG 480
DB 444 GGGGACATCAAGACATCGTGGCCATATTTCCGTTCCGCTGGTGGTCTTGTGTTCCGCTG 503
QY 481 GGTGTCTTTGTGTACCGCTGGGAACGTCGCCACAGACCCGCGGCATAGCTTCAGCTCAA 540
DB 504 GGTGTCTTTGTGTACCGCTGGGAACGTCGCCACAGACCCGCGGCATAGCTTCAGCTCAA 563
QY 541 GCACGCCAGGCGCCCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCC-CCCTC 599
DB 564 GCACGCCAGGCGCCCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCCGCGCTC 623
QY 600 AGCCGCGCTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTCTAGCATGTGGCT 659
DB 624 AGCCGCGCTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTCTAGCATGTGGCT 683
QY 660 TTAATAAATACATAAATAATGCTTTTTT 687
DB 684 TTAATAAATACATAAATAATGCTTTTTT 711

RESULT 6
US-08-954-470-1
Sequence 1, Application US/08954470
Patent No. 5876965
GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Quelle, Dawn, E.
TITLE OF INVENTION: ARF-p19, A No. 5876965el Regulator of the
TITLE OF INVENTION: Mammalian Cell Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 28-SEP-1995
CLASSIFICATION: 435
APPLICATION NUMBER: 08/534,975
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0590000
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..548
FEATURE:
NAME/KEY: CDS
LOCATION: 43..548

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; NAME/KEY: CDS
; LOCATION: 43..551
US-08-954-470-1

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Query Match	78.9%;	Score 672.8;	DB 3;	Length 713;
Best Local Similarity	99.6%;	Pred. No. 6.2e-187;		
Matches 685;	Conservative .0;	Mismatches 2;	Indels 1;	Gaps 1;

Qy	1	GGAGTACAGCAGCGGGAGCATGGTTCGCAGGTTCTTGGTCTACTGTGAAGATTACAGCGCC	60
Db	24	GGAGTACAGCAGCGGGAGCATGGTTCGCAGGTTCTTGGTACTTGCAGGATTACAGCGCC	83
Qy	61	GGCGCGCCACTCCAAAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCGGAGACCCAG	120
Db	84	GGCGCGCCACTCCNAGAGAGGGTTTCTTGGTGAAGTTCTGTCGATCCGGAGACCCAG	143
Qy	121	GACAGCGAGCTGGCGTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG	180
Db	144	GACAGCGAGCTGGCGTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAG	203
Qy	181	AAGAGGGCCACCCGGAATCCTCGACACAGGTGATGATGGCAACGTTACGTAGCAG	240
Db	204	AAGAGGGCCACCCGHAATCCTCGACACAGGTGATGATGGCAACGTTACGTAGCAG	263
Qy	241	CTCTTCTGCTCAACTACGGTGCAGATTCGAACTTCGAGGACCCCACTACTTCTCCCGCC	300
Db	264	CTCTTCTGCTCAACTACGGTGCAGATTCGAACTTCGAGGACCCCACTACTTCTCCCGCC	323
Qy	301	CGGTGCACGACGACGCGGGAGGGCTTCTCGACACGCTGGTGGTCTGCACGGGTGAG	360
Db	324	CGGTGCACGACGACGCGGGAGGGCTTCTCGACACGCTGGTGGTCTGCACGGGTGAG	383
Qy	361	GGGCTCGGCTTGTGTGCGCGATGTCCTGGGGTGCCTGCCGCTCGACTTGGCCCAAGAGC	420
Db	384	GGGCTCGGCTTGTGTGCGCGATGTCCTGGGGTGCCTGCCGCTCGACTTGGCCCAAGAGC	443
Qy	421	GGGGACATCAAGACATCGTCCGATATTGGTTCGCCGCTGGGTGCTCTTGTGTTCCGCTG	480
Db	444	GGGGACATCAAGACATCGTCCGATATTGGTTCGCCGCTGGGTGCTCTTGTGTTCCGCTG	503
Qy	481	GGTGGTCTTTGTGTACCGCTGGGAAGCTGCCCCAGACCCGACGGCATAGCTTCAAGTCAA	540
Db	504	GGTGGTCTTTGTGTACCGCTGGGAAGCTGCCCCAGACCCGACGGCATAGCTTCAAGTCAA	563
Qy	541	GCAGGCCAGGGCCCTGGAACTTTCGGGGCCAAATCCCAAGACAGAGCTAAATCC--GCCTC	599
Db	564	GCAGGCCAGGGCCCTGGAACTTTCGGGGCCAAATCCCAAGACAGAGCTAAATCCGGCCTC	623
Qy	600	AGCCCGCCTTTTCTTCTTAGCTTCACTTCTACGCGATGCTAGCGTGTCTAGCATGTGGCT	659
Db	624	AGCCCGCCTTTTCTTCTTAGCTTCACTTCTACGCGATGCTAGCGTGTCTAGCATGTGGCT	683
Qy	660	TTAAAAAATACATAATAATGCTTTTTT	687
Db	684	TTAAAAAATACATAATAATGCTTTTTT	711

RESULT 7
US-09-129-855A-1
; Sequence 1, Application US/09129855A
; Patent No. 6046032
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p13, A No. 6046032el Regulator of the Mammalian
; TITLE OF INVENTION: Cell Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.

APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: 126..127 /note= "splice site"
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: 467..468
OTHER INFORMATION: /note= "Splice site"
US-08-508-735-44

Query Match 44.0%; Score 382.2; DB 3; Length 507;
Best Local Similarity 98.0%; Pred. No. 2.6e-102;
Matches 387; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 196 GAATCTGCACAGGTGATGATGGGCAAGTTCAGGTAGCAGCTTCTGCTCAACT 255
DB 113 GTACCCGATTTCAGGTGATGATGGGCAAGTTCAGGTAGCAGCTTCTGCTCAACT 172
QY 256 ACGGTGCAGATTCGAACTCGAGAGACCCACCTTCTCCGCCCGGTGCACGACGACG 315
DB 173 ACGGTGCAGATTCGAACTCGAGAGACCCACCTTCTCCGCCCGGTGCACGACGACG 232
QY 316 CGCGGGAAGCTTCTGGACACGCTGGTGGTCTGCACGGGTGAGGGCTCGGTGGATG 375
DB 233 CGCGGGAAGCTTCTGGACACGCTGGTGGTCTGCACGGGTGAGGGCTCGGTGGATG 292
QY 376 TCGCGGATCCCTGGGTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
DB 293 TCGCGGATCCCTGGGTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
QY 436 TCGTGCATATTTGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
DB 353 TCGTGCATATTTGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
QY 496 CGCTGGGAAGCTCGCCAGACGCTGGTGGTCTGCACGGGTGAGGGCTCGGTGGATG 555
DB 413 CGCTGGGAAGCTCGCCAGACGCTGGTGGTCTGCACGGGTGAGGGCTCGGTGGATG 472
QY 556 TGAACCTTCGCGGCAATCCCAAGACGACGCTAA 590
DB 473 TGAACCTTCGCGGCAATCCCAAGACGACGCTAA 507

RESULT 10
US-08-474-177-25
Sequence 25, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERM LINE MUTATIONS IN THE MTS GENE

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-474-177-25

Query Match 44.0%; Score 375; DB 1; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGAGAGCCAGGACGCG-AGCTGC 133
DB 1 AAGAGAGGGTTTCTTGGTGAAGTTCGTCGATCCCGAGAGCCAGGACGCGTCTGC 60
QY 134 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCGGCAC 193
DB 61 GCTCTGGCTTTCTGTAACATGTTGTTAGGCTAGAGAGGATCTTGAGAGAGGGCGGCAC 120
QY 194 CGGAATCTCGGACGAGTATGATGGCAACGTTTACGTAGCAGCTTCTGCTCAA 253
DB 121 CGGAATCTCGGACGAGTATGATGGCAACGTTTACGTAGCAGCTTCTGCTCAA 180
QY 254 CTACGGTGCAGATTCGAACTGGGAGGACCCCACTACTCTCTCCCGCGGTGCAGGACG 313
DB 181 CTACGGTGCAGATTCGAACTGGGAGGACCCCACTACTCTCTCCCGCGGTGCAGGACG 240

;; FILING DATE: 14-APR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/214,582
;; FILING DATE: 18-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELEPHONE: 202-962-4810
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 395 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-480-810-25

Query Match 44.0%; Score 375; DB 2; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCG-AGCTGC 133
DB 1 AAGAGAGGTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCGTAGTGC 60

QY 134 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193
DB 61 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 120

QY 194 CGGAATCTGACAGGTTCTGCGATCCCGAGACCCAGGACGCG-AGCTGC 253
DB 121 CGGAATCTGACAGGTTCTGCGATCCCGAGACCCAGGACGCGTAGTGC 180

QY 254 CTACGGTGCAGATTCCGAACTCGAGGACCCACACCTTCTCCCGCCGGTGCACGACGC 313
DB 181 CTACGGTGCAGATTCCGAACTCGAGGACCCACACCTTCTCCCGCCGGTGCACGACGC 240

QY 314 AGCGGGGAAGGCTTCTGGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193
DB 61 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 120

QY 374 TGTCGGCATGCTGGGTCGCTGCGCTCGACTTGGCCCAAGAGGGGACATCAAGA 433
DB 301 TGTCGGCATGCTGGGTCGCTGCGCTCGACTTGGCCCAAGAGGGGACATCAAGA 360

QY 434 CATCGTGCAGATTATTTGGCTTCCGCTGGGTGCTCTT 468
DB 361 CATCGTGCAGATTATTTGGCTTCCGCTGGGTGCTCTT 395

RESULT 13
US-08-735-25
; Sequence 25, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/508,735
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US to be assigned
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/03316
;; FILING DATE: 17-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ihnen, Jeffrey L.
;; REGISTRATION NUMBER: 28,957
;; REFERENCE/DOCKET NUMBER: 24884-109348
;; TELEPHONE: 202-962-4848
;; TELEFAX: 202-962-8300
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 395 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-508-735-25

Query Match 44.0%; Score 375; DB 3; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCG-AGCTGC 133
DB 1 AAGAGAGGTTTCTTGGTGAAGTTCTGCGATCCCGAGACCCAGGACGCGTAGTGC 60

QY 134 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193
DB 61 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 120

QY 194 CGGAATCTGACAGGTTCTGCGATCCCGAGACCCAGGACGCG-AGCTGC 253
DB 121 CGGAATCTGACAGGTTCTGCGATCCCGAGACCCAGGACGCGTAGTGC 180

QY 254 CTACGGTGCAGATTCCGAACTCGAGGACCCACACCTTCTCCCGCCGGTGCACGACGC 313
DB 181 CTACGGTGCAGATTCCGAACTCGAGGACCCACACCTTCTCCCGCCGGTGCACGACGC 240

QY 314 AGCGGGGAAGGCTTCTGGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193
DB 61 GCTCTGGCTTTCGTAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 120

QY 374 TGTCGGCATGCTGGGTCGCTGCGCTCGACTTGGCCCAAGAGGGGACATCAAGA 433
DB 301 TGTCGGCATGCTGGGTCGCTGCGCTCGACTTGGCCCAAGAGGGGACATCAAGA 360

QY 434 CATCGTGCAGATTATTTGGCTTCCGCTGGGTGCTCTT 468
DB 361 CATCGTGCAGATTATTTGGCTTCCGCTGGGTGCTCTT 395

RESULT 14
US-08-848-251-25
; Sequence 25, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.

APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-G
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-848-251-25

Query Match 44.08; Score 375; DB 4; Length 395;
Best Local Similarity 98.59; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 75 AAGAGAGGTTTCTTGTGTAAGTTCTGCGATCCCGAGACCCAGGACCG-AGCTGC 133
Db 1 AAGAGAGGTTTCTTGTGTAAGTTCTGCGATCCCGAGACCCAGGACCGTAGCTGC 60
Qy 134 GCTCTGGCTTCGTAACATCTTGTGAGGCTAGAGAGGATCTTGAGAAGAGGCCCGCAC 193
Db 61 GCTCTGGCTTCGTAACATCTTGTGAGGCTAGAGAGGATCTTGAGAAGAGGCCCGCAC 120

Qy 194 CGGAATCCTGGACGAGTGATGATGGCAACGTTACGTTACGAGCTCTTCTGCTCAA 253
Db 121 CGGAATCCTGGACGAGTGATGATGGCAACGTTACGTTACGAGCTCTTCTGCTCAA 180
Qy 254 CTACGGTGCAGATTGCAACTGCGAGGACCCCACTACTCTTCCCGCCGCGTGACGACGC 313
Db 181 CTACGGTGCAGATTGCAACTGCGAGGACCCCACTACTCTTCCCGCCGCGTGACGACGC 240
Qy 314 AGCGCGGGAAGGCTTCTCTGACACGCTGGTGTGCTGACGCGGTGAGGGGCTCGGCTGGA 373
Db 241 AGCGCGGGAAGGCTTCTCTGACACGCTGGTGTGCTGACGCGGTGAGGGGCTCGGCTGGA 300
Qy 374 TGTGCGGATGCGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433
Db 301 TGTGCGGATGCGCTGGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 468
Qy 434 CATCGTGCATATTGCGTTCCGCTGGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 395
Db 361 CATCGTGCATATTGCGTTCCGCTGGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 395

RESULT 15

US-08-486-047-25
Sequence 25, Application US/08486047
Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-486-047-25

Query Match 44.0%; Score 375; DB 4; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 75 AAGAGAGGTTTTCTTGTTGAAGTTCGTCGATCCCGAGACCCAGGACGCG-AGCTGC 133
|||||
Db 1 AAGAGAGGTTTTCTTGTTGAAGTTCGTCGATCCCGAGACCCAGGACGCGTAGCTGC 60

QY 134 GCTCTGGCTTTTCGTTGAACATGTTGTGAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 193
|||||
Db 61 GCTCTGGCTTTTCGTTGAACATGTTGTGAGGCTAGAGAGGATCTTGAGAAGAGGCGCGCAC 120

QY 194 CGGAATCCTTGGACCGAGTGATGATGGGCAACGTTTACGCTAGCAGCTCTTCTGCTCAA 253
|||||
Db 121 CGGAATCCTTGGACCGAGTGATGATGGGCAACGTTTACGCTAGCAGCTCTTCTGCTCAA 180

QY 254 CTACGGTGCAGATTGCACTGCGAGGACCCCACTACCTTCTCCCGCCCGGTGCAGAGGC 313
|||||
Db 181 CTACGGTGCAGATTGCACTGCGAGGACCCCACTACCTTCTCCCGCCCGGTGCAGAGGC 240

QY 314 AGCGCGGAAGGCTTCCCTGGACACGCTGGTGTGCTGCACGGGTGAGGGGCTCGGCTGGA 373
|||||
Db 241 AGCGCGGAAGGCTTCCCTGGACACGCTGGTGTGCTGCACGGGTGAGGGGCTCGGCTGGA 300

QY 374 TGTGGCGGATGCTGGGGTTCGCTCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGA 433
|||||
Db 301 TGTGGCGGATGCTGGGGTTCGCTCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGA 360

QY 434 CATCGTGCAGATTGCGGTTCGCGTGGGTGCTCTT 468
|||||
Db 361 CATCGTGCAGATTGCGGTTCGCGTGGGTGCTCTT 395

Search completed: July 21, 2000, 06:06:41
Job time: 13807 sec

Gencore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2000, 02:48:45 ; Search time 1049.06 Seconds
(without alignments)
3585.670 Million cell updates/sec

Title: US-09-016-869A-5
Perfect score: 853
Sequence: 1 GGAGTACAGCAGCGGACCA.....GATACTTTTAAATGTCAA 853

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues 10495684
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	em_est2:*
3:	em_est3:*
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QY 334 ACACGCTGGTGTGCTGCACGGGTCAAGGGCTCGGCTGGATGTGCGGATGCCCTGGGGTC 393
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QY 394 GCGTGGCGCTCGACTTGGCCCAAGAGCGGGACATCAAGACATCGTCCGATATTTGGTT 453
Db 368 GTCTGCCGTGGACCTGGCTGAGAGCTGGGCGCATCGCATGTCGACGCTACTCGCG 309
QY 454 CGCTGGGGTG 463
Db 308 CGGCTGGGG 299

RESULT 2
AI363262/c
LOCUS
DEFINITION
  qv56f03.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3'
  similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains
  LTR9.b3 TAR1 repetitive element ; , mRNA sequence.
ACCESSION
  AI363262
VERSION
  AI363262.1 GI:4114883
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 708)
  NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute / National Institute of Neurological
  Disorders and Stroke, Brain Tumor Genome Anatomy Project
  (CGAP/BrGAP), Tumor Gene Index
  Unpublished (1998)
JOURNAL
  Contact: Robert Strausberg, Ph.D.
  Tel: (301) 496-1550
  Email: Robert.Strausberg@nih.gov
  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
  Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
  Bonaldo, Ph.D.
  cDNA Sequencing by: Greg Lennon, Ph.D.
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 872 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 394.
FEATURES
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    1..708
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2016029"
    /clone_lib="NCI-CGAP_Brn23"
    /tissue_type="glioblastoma (pooled)"
    /lab_host="DH10B"
    /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
    modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
    strand cDNA was primed with a Not I - oligo(dT) primer [5'
    TGTACCAATCTGAAGTGGGAGCGCGCGGCTATCTTTTCTTTTCTTTTCTTTT
    T 3']; double-stranded cDNA was ligated to Eco RI
    adaptors (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of the modified pT7T3 vector.
    Library is normalized, and was constructed by Bento
    Soares and M.Fatima Bonaldo."
  BASE COUNT 137 a 210 c 219 g 140 t 2 others
ORIGIN
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QY 41 ACTGTAAGATTACAGCGCGGGCCGCCCTCCACAGAGAGGGTTTCTTGGTGAAGTTC 100
Db 708 ACCCTCGGAATTCGGCGCGCGTTCGGCCCGCGCGAGTAGGGG-TTTCGTTGGTTCATC 650
QY 101 GTCGGATCCGGAGACCCAGGACAGCGAGTGGCTTCTGCTGAACATGTTGTTG 160
Db 649 CACAGTCACTACNGGGAGTGGCGAGCGCGAGGGGCGCCGCCCTGTGGCTTCGTGCTG 590
QY 161 AGCTAGAGAGATCTTTGAGAAGAGGGGCGCCACCGGAATCCTG---GACCAGGTGATGAT 217
Db 589 ATGCTACTAGAAAGCCAGCGTCTAGGCGAGCAGCCGCTTCTCTAGAGAGCAGGTCTATGAT 530
QY 218 GATGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGCTGAGATTCGAACTCGGA 277
Db 529 GATGGCAAGCGCCCGAGTGGCGAAGCTGTGCTGCCGGGCGCGAGGCCCAACTGCGA 470
QY 278 GGACCCCACTACCTTCTCCCGCGCTGCACGACGACGCGGGAAGGCTTCTCTGGACAC 337
Db 469 CGACCCCGCAACTCTACCCGACCCCTGCACGACGCTGCCGGGAGGGCTTCTCTGGACAC 410
QY 338 GCTGGTGGTGTGTCACGGGTCAAGGGCTCGGCTGGATGTGCGGATGCCCTGGGGTCCCT 397
Db 409 GCTGGTGGTGTGTCACCGGGCGCGGGCTGGAGCTGCGGATGCCCTGGGGCGGTCT 350
QY 398 GCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGGGATATTTCGTTCCGC 457
Db 349 GCGCTGGACCTGGCTGAGAGAGCTGGGCGCATCGCGATGTGCGACGTTACCTGCGCGGC 290
QY 458 TGGGTG 463
Db 289 TGGGG 284

RESULT 3
AI328496
LOCUS
DEFINITION
  ds02hl2.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
  sequence.
ACCESSION
  AI328496
VERSION
  AI328496.1 GI:6798992
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 648)
  NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
JOURNAL
  On Apr 7, 1998 this sequence version replaced gi:3036295.
  Contact: Robert Strausberg, Ph.D.
  Tel: (301) 496-1550
  Email: Robert.Strausberg@nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: Edge BioSystems
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Plate: LLC0030 row: 0 column: 24
  Seq primer: -21M13 forward primer (ABI).
FEATURES
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    1..648
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:2847599"
    /clone_lib="NIH_MGC_4"
    /cell_line="MGC1"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: Cervix; Vector: pOTB7a; Site_1: ScaI;
    Site_2: CeuI; cDNA made by oligo-dT priming."
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Directionally cloned into Ceul/SeeI sites using the following 5' adaptor: taactaacgtctctagtagcga and 3' adaptor: ttctattacctcttctcgacccacataaa. Average insert size 900 bp. Library prepared by Edge Biosystems.

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BASE COUNT      127 a   200 c   196 g   123 t     2 others
ORIGIN

Query Match      20.6%; Score 175.8; DB 71; Length 648;
Best Local Similarity 71.2%; Pred. No. 4.1e-38;
Matches 247; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

Qy 120 GGACAGCAGCTGCGCTCTGCTTCTCGTGAACATGTTTGTAGAGCTAGAGAGGATCTTGA 179
Db 19 GGGCAGCCAGGGGCGCCCGCTGCGCTCTGCTGATGCTACTGAGGAGCCAGC 78

Qy 180 GAAGAGGCGCCGACCGGAATCT---GGACCAGGTGATGATGGGCAACGTTACGTA 236
Db 79 GTCTAGGGCAGCAGCGCTTCTTGAAGACCAGGTGATGATGGGCGGCCGCGAGTG 138

Qy 237 GCAGCTCTTCTTCAACTACGGTGCAGATTCGAATCCGAGGACCCCACTACCTTCTCC 296
Db 139 GCGAGCTGCTGCTCTCCAGCGCGGAGCCCACTGCGCGACCCGCGCACTCTCACC 198

Qy 297 GCGCGGTGCAGCAGCAGCGCGGAGGCTTCTTGACAGCTGTGTGTGTCGACGGG 356
Db 199 GCACCGTGCACGAGCTGCGCGGAGGCTTCTTGGACACGCTGTGTGTGTCGACCGG 258

Qy 357 TCAGGGCTCGGCTGGATGTCGGCGATGCTGCGGTCGCGCTGCGCTGCGCTGCGG 416
Db 259 GCGGGGCGGCTGGAGCTGCGGATGCTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGG 318

Qy 417 GAGCGGGACATCAAGACATCGTGCATATTGCGTTCGCTGCGTGGGTG 463
Db 319 GAGCTGGCCATCGGATGTCGACGTTACCTGCGCGCGGTGCGGG 365

RESULT 4
AI765096/c 774 bp mRNA EST 21-DEC-1999
LOCUS w148b08.x1 NCI.CGAP.Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
DEFINITION similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN; contains
LN9.83 MER22 repetitive element ;, mRNA sequence.
ACCESSION AI765096
VERSION AI765096.1 GI:5231605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL On Feb 22, 1999 this sequence version replaced gi:4283180.
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 400.
Location/Qualifiers
1. 774

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/clone_lib="NCI.CGAP.Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI.CGAP.Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-106125, and 114584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaudo. "
BASE COUNT      153 a   220 c   221 g   179 t     1 others
ORIGIN

Query Match      19.4%; Score 165.6; DB 44; Length 774;
Best Local Similarity 66.9%; Pred. No. 2.8e-35;
Matches 295; Conservative 0; Mismatches 140; Indels 6; Gaps 4;

Qy 29 AGTCTTCTGCTCACTGTAAGGATTCAGCGCGCGCGCCCACTCCAGAGAGGGTTTC 88
Db 774 AGGTTCTGGTGAATTCGGGATTCGGGCGCGCGGCCCGCCGAAAGTTAGGGTTTC 715

Qy 89 TTGG-TGAAGTTGTCGATCCCGGAGACCCAGACAGCAGCTGCGC-TCTGGCTTTCG 146
Db 714 GTGGTTACATCCCGGGCTCACGGGGAGGTGGCAGCGCGCGCCCGCTGT 655

Qy 147 TGAACATGTTGTAGGCTAGAGAGGA-TCTTTGAGAAGAGGCGCCGACCGAATCT--- 202
Db 654 GGGCCATCTGCTTATGCTATTAGGAGAGCCAGCGCTTTAGGAGCAGCAGCGCTTCTCTAGA 595

Qy 203 GGACAGGTGATGATGGGCAACGTTCACTGACGCTCTTCTGCTCACTACGTTGC 262
Db 594 AGACAGGTGATGATGGGCGAGCGCGGAGTGGCGAGCTGCTGCTCCACGCGCGC 535

Qy 263 AGATTGCAACTCGGAGACCCCACTACCTTCTCCGCGCGGTGACGACGAGCGCGGA 322
Db 534 GGAGCCCAATTTGGCGCGACCCCGCCACATTTACCCGACCGTGCACGAGCTGCCCGGA 475

Qy 323 AGCTTCTTGACAGCTGTGTGCTGCTGACGGGTGAGGGCTCGGCTGAGTGCAGGA 382
Db 474 GGGCTTCTTGGACAGCTGTGTGCTGCTGACCGGGCGCGCGCTGAGTGCAGGA 415

Qy 383 TGCTGGGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 442
Db 414 TGCTGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 355

Qy 443 ATATTGCGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 463
Db 354 GTACCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334

RESULT 5
AI765096/c 590 bp mRNA EST 07-MAR-2000
LOCUS w181d11.x1 NCI.CGAP.Br25 Homo sapiens cDNA clone IMAGE:2431317 3'
DEFINITION similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; , mRNA sequence.
ACCESSION AI765096
VERSION AI765096.1 GI:5545430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS NCI/NINDS-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
```

JOURNAL
COMMENT
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.

SOURCE

human.
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 579)

REFERENCE

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/hcigap>.

AUTHORS

National Cancer Institute / National Institute of Neurological

TITLE

Disorders and Stroke, Brain Tumor Genome Anatomy Project

JOURNAL

Unpublished (1998)

COMMENT

On May 18, 1998 this sequence version replaced gi:3136859.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 819 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 474.

FEATURES

source

1..579

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2430933"

/clone_lib="NCI-CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT

113 a 157 c 182 g 127 t

ORIGIN

Query Match

Best Local Similarity

Matches 196; Conservative

0; Mismatches 64; Indels 0; Gaps 0;

18.5%; Score 157.6; DB 45; Length 579;

75.4%; Pred. No. 4.2e-33;

Query 204 GACCAGTGTATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCA 263

Db 558 GACCAGTGTATGATGGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCG 499

Query 264 GATTCGACTGCGAGGACCCCACTACCTTCTCCGCGCGGCGGCGGCGGAA 323

Db 498 GAGCCCAACTGCGCGAGGACCCCACTACCTTCTCCGCGCGGCGGCGGCGGAG 439

Query 324 GGCTTCTCGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 383

Db 438 GGCTTCTCGACACGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 379

Query 384 GCCTGGGGTCCGCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTCGA 443

Db 378 GCCTGGGGTCCGCTGCGGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTCGA 443

Query 444 TATTCGCTTCCGCTGGGTG 463

Db 318 TACCTGCGCGGCTGCGGG 299

RESULT 7

JOURNAL
COMMENT
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.

SOURCE

human.
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 579)

REFERENCE

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/hcigap>.

AUTHORS

National Cancer Institute / National Institute of Neurological

TITLE

Disorders and Stroke, Brain Tumor Genome Anatomy Project

JOURNAL

Unpublished (1998)

COMMENT

On May 18, 1998 this sequence version replaced gi:3136859.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 845 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 444.

FEATURES

source

1..590

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2431317"

/clone_lib="NCI-CGAP_Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT

114 a 158 c 179 g 139 t

ORIGIN

Query Match

Best Local Similarity

Matches 204; Conservative

0; Mismatches 73; Indels 0; Gaps 0;

18.8%; Score 160.2; DB 45; Length 590;

73.6%; Pred. No. 8.1e-34;

Query 187 GCCGACCGGAATCTCGACAGGTGATGATGGGCAACGTTACGTAGCAGCTTTC 246

Db 586 GCAGCCGCTTCATAGAACAGCAGGTCTGATGGGCGAGCGCCAGAGTGGCGGAGTGC 527

Query 247 TGCTCAACTAGCGTGCAGATTTCGAACGCGAGGACCCCACTACCTTCTCCGCGCGGCGTC 306

Db 526 TGCTGCTCCAGCGCGGAGCCCACTGCGCGGACCCCGCCACTCTCACCGACCCGTCG 467

Query 307 ACAGCAGCGCGCGGAGAGGCTTCTCGACAGCGTGGTGGTGGTGGTGGTGGTGGTGG 366

Db 466 ACAGCAGCGCGCGGAGAGGCTTCTCGACAGCGTGGTGGTGGTGGTGGTGGTGGTGG 407

Query 367 GGCTGGATGTCGCGATGCTGGGGTGGCTGGCGCTGGCTGGCTGGCTGGCTGGCTGG 426

Db 406 GGCTGGATGTCGCGATGCTGGGGTGGCTGGCGCTGGCTGGCTGGCTGGCTGGCTGG 347

Query 427 ATCAAGACATCGTCCGATATTTGGTTCCTGGCTGGCTGGCTGGCTGGCTGGCTGG 463

Db 346 ATCCGATGTCGACAGGTACCTGCGCGGCGTGGCGG 310

RESULT 6

AI870879/c

LOCUS

DEFINITION

AI870879

VERSION

AI870879.1

KEYWORDS

AI870879 579 bp mRNA EST 07-MAR-2000
w177d11.x1 NCI-CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2430933 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
AI870879
AI870879.1 GI:5544847
EST.

AI362049/c
LOCUS AI362049 580 bp mRNA EST 15-FEB-1999
DEFINITION qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ; mRNA sequence.
ACCESSION AI362049
VERSION AI362049.1 GI:4113670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 580)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 321.
Location/Qualifiers
1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 116 a 160 c 174 g 130 t
ORIGIN
Query Match 18.5%; Score 157.6; DB 38; Length 580;
Best Local Similarity 75.4%; Pred. No. 4.2e-33;
Matches 196; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 204 GACCAGGTGATGATGGGCAAGCTTCACGTAGCAGCTCTTCCTCACTACGAGTGC 263
DB 559 GACCAGGTGATGATGGGCGAGCGCTGAGTGGGAGCTGCTGCTCCACGGCGG 500
QY 264 GATTGCAACTGGAGAGCCCACTACCTTCTCCCGCCGGTGCACGACGACGCCGGAA 323
DB 499 GAGCCCACTGGCGGACTCCGCCACTCTACCCGGAACCGTGCACGAGCTGCCGGAG 440
QY 324 GGCTCTCTGGACAGCTGGTGGTCTGCACGGGTGAGGGGCTCGGCTGGATGCGCGAT 383
DB 439 GGCTTCTTGAACAGCTGGTGGTGGTGCACCGGGCGGGCGGCTGGAGTGGCGGAT 380
QY 384 GCCTGGGCTGCGCTGCCCTCGACTTGGCCCAAGAGGGGGGACATCAAGACATCGTCGA 443
DB 379 GCCTGGGCGCTGCTGCCGTGGACCTGGCTGAGGAGCTGGGCCATCGGATGTCGACGG 320

QY 444 TATTTCCGTTCCGCTGGGTG 463
DB 319 TACCTCGCGCGCTGCGGG 300
RESULT 8
LOCUS AI394605 566 bp mRNA EST 30-MAR-1999
DEFINITION tgl13q05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A ; contains LTR9.b3 TAR1 repetitive element ; mRNA sequence.
ACCESSION AI394605
VERSION AI394605.1 GI:4224152
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 566)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 755 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
1..566
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2108696"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphocytic leukemia"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATGCTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 113 a 159 c 175 g 118 t
ORIGIN
Query Match 18.4%; Score 156.6; DB 39; Length 566;
Best Local Similarity 73.9%; Pred. No. 8e-33;
Matches 198; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 196 GAATCCTGGACAGGTGATGATGGGCAAGCTTCACGTAGCAGCTCTTCGCTCAACT 255
DB 559 GGAGGCCGATCCAGGTGATGATGGGCGAGCGCGGAGCTGCTGCTGCC 500
QY 256 AGGTTGCAGATTCGAACTCGGAGAGCCCACTACCTTCTCCCGCCGGTGCACGACGAG 315
DB 499 ACGGCGGAGGCCCACTGCGCNGACCCCGCCACTCTCACCGACCCGTCACGACGCTG 440
QY 316 CGCGGGAAGGCTTCTTGGACAGCTGGTGGTGTCTGCACGGGTGAGGCTCGGCTGGATG 375


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/db_xref="taxon:9606"
/clone="IMAGE:2242122"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1459084-1470983, and 1475392-1476743). Subtraction by
Bento Soares and M. Fatima Bonaudo."
BASE COUNT      107 a 144 c 163 g 116 t      1 others
ORIGIN

Query Match      16.3%; Score 139.4; DB 42; Length 531;
Best Local Similarity 75.2%; Pred. No. 4.4e-28;
Matches 173; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 234 GTACGAGCTCTTCTCACTACGGTGCAGATTTCGAACCTGCGAGGACCCACTACTTC 293
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 528 GTGGCGAGCTGCTGCTCCAGCGCGGAGGCCCAACTGCGCGACNCCGCACTCTC 459
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 294 TCCGCGCGGCTGACGACGCGGAGAGGCTTCTTGACACAGCTGTGTGCTGCAC 353
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 468 ACCGACCCGTCAGCAGCTGCTGCCGCGGAGGCTTCTTGACACAGCTGTGTGCTGCAC 409
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 354 GGGTCAGGGCTCGGCTGGATGTCGGCGATGCTGGGGTGCCTTGGCTGCGTCTGGGCC 413
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 408 CGGGCGGGCGCGCTGGAGCTGCGGATGCTGGGGCGGCTGCGCGTGGACCTGGCT 349
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 414 CAAGAGCGGGACATCAAGACATCGTCGATATTGCTTCGCTGGGTG 463
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 348 GAGGAGCTGGGCCATCGGATGTCGACAGTACTGCGCGCGCTGCGGG 299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
AW631047      480 bp mRNA EST      31-MAR-2000
LOCUS      hn91d11.y1 NCI_CGAP_GUI Homo sapiens cDNA clone IMAGE:2970165 5'
DEFINITION      Similar to SW:CDN2.HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; mRNA sequence.
ACCESSION      AW631047
VERSION      AW631047.1 GI:7377837
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 480)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      On Jan 6, 2000 this sequence version replaced gi:6676951.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 314.
Location/Qualifiers
1. .480
FEATURES
source
```

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2970165"
/clone_lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: Sali; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."
BASE COUNT      94 a 144 c 135 g 107 t
ORIGIN

Query Match      15.6%; Score 133.4; DB 79; Length 480;
Best Local Similarity 74.9%; Pred. No. 2e-26;
Matches 167; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 207 CAGGTGATGATGGGCAACGTTTACGTAGCAGCTCTTCTGCTCAACTACGGTGCAGAT 266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 CAGGTGATGATGGGCAAGCGCCGCTGGCGAGCTGCTGCTCCACGCGCGGAG 315
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 267 TCGAACTGGGAGGACCCACTACCTTCTCCCGCGGTGGTGCAGCAGCGCGGAGGC 326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 CCCAACTGGCAGACCCCTGCCACTCTCACCGCAGCGGTGCATGATGCTCCCGGAGGGC 375
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 327 TTCCCTGGACAGCTGGTGTGCTGCACGGGTGTCAGGGGCTCGGCTGGATGTGCGCGATGCC 386
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 TTCCCTGGACAGCTGGTGTGCTGTACCGTCCCGGGCGCGCTTGACGTGCACACTATGCT 435
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 387 TGGGTCGCCCTGCCCTCGACTTGGCCCCAAGAGCGGGGACATC 429
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 CTGGGTCTGCTGCCCATAGACTTGTCCGAAGAAGTGGGTCAAC 478
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: July 21, 2000, 02:48:50
Job time: 9645 sec
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MPSRELH

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:41:29 2000; MasPar time 6.47 Seconds
457.636 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-6
Description: (1-125) from US09016869A.pep
Perfect Score: 892
Sequence: 1 MMGNVHVALLNYGADSN.....SFSSSTPRALELRGQSQEQS 125

Scoring table: PAM 150
Gap 11

Searched: 189963 seqs, 23586106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq36
1:geneseq

Statistics: Mean 29.993; Variance 124.567; scale 0.241

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	892	100.0	125	1 W16322	Murine INK4a-p16 C-ter	3.05e-77
2	892	100.0	125	1 R85120	Cell-cycle regulatory	3.05e-77
3	892	100.0	168	1 W80527	Mouse multiple tumour	3.05e-77
4	723	81.1	127	1 R85119	Cell-cycle regulatory	3.90e-60
5	473	53.0	105	1 W80525	A human multiple tumou	3.94e-35
6	473	53.0	105	1 R81700	Multiple tumour suppre	3.94e-35
7	473	53.0	105	1 W74550	Amino acid sequence 1	3.94e-35
8	473	53.0	105	1 R80947	Human multiple tumour	3.94e-35
9	473	53.0	105	1 W19254	Human multiple tumour	3.94e-35
10	473	53.0	105	1 W40525	Human MTS1E1-beta prot	3.94e-35
11	473	53.0	148	1 R81701	Multiple tumour suppre	3.94e-35
12	473	53.0	148	1 R80940	Human multiple tumour	3.94e-35
13	473	53.0	151	1 R53401	Inhibitor of cyclin de	3.94e-35
14	473	53.0	156	1 W74549	Amino acid sequence of	3.94e-35
15	473	53.0	156	1 R85116	Cell-cycle regulatory	3.94e-35
16	473	53.0	156	1 W10627	Tumour suppressor p16.	3.94e-35
17	473	53.0	156	1 W80524	A human multiple tumou	3.94e-35
18	473	53.0	156	1 W19251	Human multiple tumour	3.94e-35
19	473	53.0	156	1 W40524	Human MTS1 protein.	3.94e-35
20	473	53.0	237	1 W95105	Truncated p27/p16 fusi	3.94e-35
21	473	53.0	252	1 W95106	Truncated p27/p16 fusi	3.94e-35
22	473	53.0	334	1 W95103	Truncated p27/p16 fusi	3.94e-35
23	473	53.0	365	1 W95107	Human p16p27 fusion pr	3.94e-35

24	473	53.0	365	1 W95096	Human p16p27 fusion pr	3.94e-35
25	473	53.0	365	1 W23536	CDK inhibitory fusion	3.94e-35
26	473	53.0	380	1 W23535	CDK inhibitory fusion	3.94e-35
27	473	53.0	380	1 W95095	Human p16(GS)p27 fusio	3.94e-35
28	473	53.0	391	1 W95094	Human p27-p16 fusion p	3.94e-35
29	473	53.0	391	1 W23534	CDK inhibitory fusion	3.94e-35
30	472	52.9	138	1 W74553	Amino acid sequence 2	4.95e-35
31	472	52.9	138	1 W40526	Human MTS2 protein.	4.95e-35
32	472	52.9	138	1 R81702	Multiple tumour suppre	4.95e-35
33	472	52.9	138	1 W19255	Human multiple tumour	4.95e-35
34	472	52.9	138	1 W80526	A human multiple tumou	4.95e-35
35	472	52.9	138	1 R80948	Human multiple tumour	4.95e-35
36	464	52.0	156	1 W19252	Human multiple tumour	3.05e-34
37	461	51.7	130	1 W70823	Mouse multiple tumour	6.04e-34
38	460	51.6	138	1 R85117	Cell-cycle regulatory	7.59e-34
39	459	51.5	130	1 R85118	Cell-cycle regulatory	9.52e-34
40	456	51.1	156	1 W19253	Human multiple tumour	1.88e-33
41	453	50.8	348	1 W95104	Truncated p27/p16 fusi	3.72e-33
42	439	49.2	85	1 R85113	Cell-cycle regulatory	8.93e-32
43	439	49.2	138	1 R85115	Cell-cycle regulatory	8.93e-32
44	439	49.2	157	1 R85114	Cell-cycle regulatory	8.93e-32
45	396	44.4	67	1 W16324	Human INK4a-p16 C-term	1.48e-27

ALIGNMENTS

RESULT 1
ID W16322 standard; Protein; 125 AA.
AC W16322;
DT 16-AUG-1997 (first entry)
DE Murine INK4a-p16 C-terminal fragment.
KW INK4a-p16; cyclin D-dependent Kinase; CDK4; CDK6; retinoblastoma;
KW cancer; tumour; ARF-p19; alternative reading frame; cell cycle;
KW therapy; wound healing.
OS Mus musculus.
PN W09712060-A1.
PD 03-APR-1997.
PF 25-SEP-1996; U15312.
PR 27-SEP-1995; US-534975.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PI Quelle DE, Sherr CJ;
DR WPI: 97-212919/19.
DR N-PSDB; T62485.
PT Nucleic acid encoding ARF-p19 which induces cell cycle arrest when
overexpressed - used for diagnosis and treatment of cancer, and for
drug screening
PS Example 1; Fig 1; 49pp; English.
CC A polypeptide (W16322) comprises the C-terminal region of murine
INK4a-p16, a specific inhibitor of the cyclin D-dependent kinases
CDK4 and CDK6. The partial polypeptide sequence is encoded by
exon 2 (see also T62485) of the INK4A gene. An syntactically
overlapping reading frame, also including exon 2, has been
identified that codes for a novel protein, ARF-p19 (W16321),
which induces cell cycle arrest when overexpressed. INK4a-p16
can block CDK4 and CDK6 from phosphorylating the retinoblastoma
protein (pRb), preventing exit from the G1 phase of the cell
cycle. Deletions and mutations involved the INK4A gene occur
frequently in cancer cells, suggesting that INK4a-p16
suppresses tumour formation.
SQ Sequence 125 AA;

Query Match 100.0%; Score 892; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.05e-77;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	MMGNVHVALLNYGADSNCEPTTFSPVHDAAREGFLDTLVHLHSGARLDVRDAG	60
QY	1	MMGNVHVALLNYGADSNCEPTTFSPVHDAAREGFLDTLVHLHSGARLDVRDAG	60
Db	61	RLPLDLAQRGHQDHYVYLRSGACSLCSAGWSLCTAGNAQTGDHFSFSSSTPRALELRQ	120
QY	61	RLPLDLAQRGHQDHYVYLRSGACSLCSAGWSLCTAGNAQTGDHFSFSSSTPRALELRQ	120

Db 121 SOEQS 125
QY 121 SOEQS 125

RESULT 2

ID R85120 standard; Protein; 125 AA.
AC R85120;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein p13.5.
KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
KW CCR; cancer; cell proliferation.
OS Mus sp.
FN W09528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
FI N-PSDB; T02965.
DR N-PSDB; T02965.
PT New cell cycle regulating proteins bind to cyclin dependent kinase -
PT and related nucleic acids, antibodies etc., used in diagnosis and
PT therapy of abnormal cell proliferation, degeneration etc.
PS Example 5; Page 81; 109pp; English.
CC The mouse cell-cycle regulatory (CCR) protein p13.5 (R85120) was
CC obd. by expression of a cDNA clone (T02965) isolated from
CC mouse embryonal stem cells. CCR p13.5 specifically inhibits the
CC activity of cyclin-dependent kinases during various stages of the
CC cell cycle, and can be used in the treatment and diagnosis of
CC proliferative disorders.
SQ Sequence 125 AA;

Query Match 100.0%; Score 892; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.05e-77;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60
Db 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
QY 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
Db 121 SOEQS 125
QY 121 SOEQS 125

RESULT 3

ID W80527 standard; Protein; 168 AA.
AC W80527;
DT 03-FEB-1999 (first entry)
DE Mouse multiple tumour suppressor 1 (MTS1) protein.
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer.
OS Mus musculus.
FN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
DR N-PSDB; V70623.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 7; Fig 19; 80pp; English.
CC The present sequence represents mouse multiple tumour suppressor 1

CC (MTS1) gene. The MTS1 gene can be used to design primers to
CC detect abnormalities i.e. polymorphisms which may predispose
CC towards malignancies such as melanoma, leukaemia, astrocytoma,
CC lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.

SQ Sequence 168 AA;

Query Match 100.0%; Score 892; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.05e-77;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 103
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVHGSGARLDVRDAG 60
Db 104 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 163
QY 61 RLPLDLAQRGHQDIVRYLRSAGCSLCAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
Db 164 SOEQS 168
QY 121 SOEQS 125

RESULT 4

ID R85119 standard; Protein; 127 AA.
AC R85119;
DT 01-MAR-1996 (first entry)
DE Cell-cycle regulatory protein homologue.
KW Cell-cycle regulatory protein; cyclin-dependent kinase inhibitor;
KW CCR; cell proliferation; agonist; antagonist.
OS Synthetic.

FH Key Location/Qualifiers
FT misc_difference 5. .7 /note= "unidentified amino acids"
FT misc_difference 10 /note= "unidentified amino acid"
FT misc_difference 14. .15 /note= "unidentified amino acids"
FT misc_difference 18. .19 /note= "unidentified amino acids"
FT misc_difference 22 /note= "unidentified amino acid"
FT misc_difference 25 /note= "unidentified amino acid"
FT misc_difference 27. .29 /note= "unidentified amino acids"
FT misc_difference 49. .50 /note= "unidentified amino acids"
FT misc_difference 65 /note= "unidentified amino acid"
FT misc_difference 69 /note= "unidentified amino acid"
FT misc_difference 71 /note= "unidentified amino acid"
FT misc_difference 74 /note= "unidentified amino acid"
FT misc_difference 76. .78 /note= "unidentified amino acids"
FT misc_difference 82 /note= "unidentified amino acid"
FT misc_difference 84 /note= "unidentified amino acid"
FT W09528483-A1.
PD 26-OCT-1995.
PF 14-APR-1995; U04636.
PR 14-APR-1994; US-227371.
PR 25-MAY-1994; US-248812.
PR 14-SEP-1994; US-306511.
PR 29-NOV-1994; US-346147.
PA (COLD-) COLD SPRING HARBOR LAB.
PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
FI WPI; 95-373798/48.

PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.
 PS Disclosure; Page 4; 109pp; English.
 CC Cell-cycle regulatory (CCR) proteins (R85116-18, R85120) have the
 CC general formula given in R85119. The CCR proteins specifically
 CC bind to cyclin-dependent kinases and function as either agonists
 CC or antagonists of cell cycle regulation.
 SQ Sequence 127 AA;

Query Match 81.1%; Score 723; DB 1; Length 127;
 Best Local Similarity 81.1%; Pred. No. 3.90e-60;
 Matches 103; Conservative 0; Mismatches 22; Indels 2; Gaps 2;
 Db 1 MMGMXXXVAXLLXGAXXNCXDPYXXRPVHDAAREGFDTLVLHXXGARDVDRDAW 60
 QY 1 MMGMNVHVAALLNYGADSNCEPTFTFS-RPVHDAAREGFDTLVLHXXGARDVDRDAW 59
 Db 61 GRLPXDAXEXGHXXLYRXGCSLCSAGWSLCTAGNVAOTDGHSSSTPRALELR 120
 QY 60 GRPLDLAQRGHQDIVRYLRSR-A-GCSLCSAGWSLCTAGNVAOTDGHSSSTPRALELR 118
 Db 121 GQSQEQS 127
 QY 119 GQSQEQS 125

RESULT 5
 ID W80525 standard; Protein; 105 AA.
 AC W80525;
 DT 03-FEB-1999 (first entry)
 DE A human multiple tumour suppressor 1E1-beta protein.
 KW Human; multiple tumour suppressor 1 gene; MTS1; cancer.
 OS Homo sapiens.
 PN US843756-A.
 PD 01-DEC-1998.
 PF 28-JUL-1995; 058735.
 PR 28-JUL-1995; US-508735.
 PR 07-JUN-1995; US-487033.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Jiang P, Kamb A, Stone S;
 DR WPI: 99-044585/04.
 DR N-PSDB; V70594.
 PT Mouse multiple tumour suppressor gene segment - useful for primer design
 PS Example 8; Fig 12A-B; 80pp; English.
 CC The present sequence represents human multiple tumour suppressor 1E1-beta
 CC (MTS1E1-beta) protein. Primers designed from the gene can be used to
 CC design primers to detect abnormalities i.e. polymorphisms which may
 CC predispose towards malignancies such as melanoma, leukaemia,
 CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
 CC thyroid, pancreas, uterus and kidneys.
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
 Db 1 MMGMARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVLRHAGARDVDRDAW 60
 QY 1 MMGMNVHVAALLNYGADSNCEPTFTFSRPVHDAAREGFDTLVLRHAGARDVDRDAW 60
 Db 61 RLPVDLAEEIGHEDVARYLRAAA 83
 QY 61 RLPDLAQRGHQDIVRYLRSAG 83

RESULT 6
 ID R81700 standard; Protein; 105 AA.
 AC R81700;
 DT 08-MAY-1996 (first entry)
 DE Multiple tumour suppressor 1 exon 1 beta (MTS1E1beta) polypeptide.
 KW Multiple tumour suppressor; MTS1E1beta; cancer; diagnosis; assay;

KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
 KW pancreas; breast; thyroid; exon 1.
 OS Homo sapiens.
 PN WO9525813-A1.
 PD 28-SEP-1995.
 PF 17-MAR-1995; U03537.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215087.
 PR 18-MAR-1994; US-215086.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR (MYRI-) MYRIAD GENETICS INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI: 95-344626/44.
 DR N-PSDB; T00744.
 PT Detecting polymorphism associated with cancer pre-disposition - also
 PT DNA, vectors and host cells e.g. for gene or protein replacement
 PT therapy and drug screening
 PS Example 7; Page 101; 148pp; English.
 CC An individual can be diagnosed as having a predisposition to cancer
 CC by detecting an alteration in the wild type multiple tumour
 CC suppressor (MTS) gene, using gene probes which hybridise to the
 CC MTS1E1beta gene ORF T00744 (which encodes R81700). The above assay
 CC can also be used in the diagnosis and prognosis of melanoma,
 CC lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
 Db 1 MMGMARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVLRHAGARDVDRDAW 60
 QY 1 MMGMNVHVAALLNYGADSNCEPTFTFSRPVHDAAREGFDTLVLRHAGARDVDRDAW 60
 Db 61 RLPVDLAEEIGHEDVARYLRAAA 83
 QY 61 RLPDLAQRGHQDIVRYLRSAG 83

RESULT 7
 ID W74550 standard; Protein; 105 AA.
 AC W74550;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence 1 of the multiple tumour suppressor MTS1E1S.
 KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
 KW somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PF 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PR (MYRI-) MYRIAD GENETICS INC.
 PA Kamb A;
 DR WPI: 98-494842/42.
 DR N-PSDB; V53830.
 PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 PT useful as hybridisation probes, primers and recombinant production
 PT of MTS in the diagnosis and treatment of cancers related to MTS
 PT mutation(s)
 PS Example 7; Column 75-76; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor
 CC (MTS1E1S) protein, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations

CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
 Db 1 MMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVLRAGARLDVRDANG 60
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60
 Db 61 RLPVDLAELGHRDVARYLRAAA 83
 QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

RESULT 8

ID R80947 standard; Protein; 105 AA.
 AC R80947;
 DT 03-MAY-1996 (first entry)
 DE Human multiple tumour suppressor polypeptide, MTS1E1-beta.
 KW Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia;
 KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
 KW gene therapy; chronic.
 OS Homo sapiens.
 PN WO9525429-A1.
 PD 28-SEP-1995.
 PF 17-MAR-1995; U03316.
 PR 18-MAR-1994; US-214581.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 95-344401/44.
 DR N-PSDB; Q99164.
 PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences
 PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.
 PT melanoma or leukaemia

PS Claim 5; Page 101; 156pp; English.
 CC Several multiple tumour suppressor (MTS) polypeptides have been isolated
 CC and sequenced. This sequence is the MTS polypeptide MTS1E1-beta.
 CC MTS polypeptide-encoding cDNAs and mutants of these are useful for
 CC the diagnosis or prognosis of human cancer. Germ-line mutations of
 CC MTS cDNAs can be used for diagnosing predisposition to melanoma,
 CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's
 CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,
 CC testis, kidney, stomach and rectum. The wild-type gene is useful
 CC for gene therapy and MTS polypeptides may also be used for protein
 CC replacement therapy. Also the polypeptides or cells contg. an
 CC altered MTS gene are useful for screening for potential cancer
 CC therapeutics.
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
 Db 1 MMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVLRAGARLDVRDANG 60
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60
 Db 61 RLPVDLAELGHRDVARYLRAAA 83
 QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

RESULT 9

ID W19254 standard; Protein; 105 AA.
 AC W19254;
 DT 10-SEP-1997 (first entry)
 DE Human multiple tumour suppressor 1 Elbeta gene product.
 KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
 KW Elbeta.
 OS Homo sapiens.
 PN US5624819-A.
 PD 29-APR-1997.
 PF 18-MAR-1994; 214582.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03537.
 PR 07-JUN-1995; US-474177.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI (UTAH) UNIV UTAH RES FOUND.
 PI Cannon-Albright LA, Kamb A, Skolnick MH;
 DR WPI; 97-258217/23.
 DR N-PSDB; T69780.
 PT Human mutant multiple tumour suppressor gene sequences - for
 PT production of recombinant mutant polypeptide(s)
 PS Disclosure: Columns 73-74; 72pp; English.
 CC The present sequence the human multiple tumour suppressor 1
 CC (MTS1) Elbeta gene product, useful in cancer diagnosis.
 SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 1 MMGSAVVAELLHGAEPNCADPATITRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60

QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVLRHSGARLDVRDANG 60

Db 61 RLPVDLAELGHRDVARYLRAAA 83

QY 61 RLPLDLAQERGHQDIVRYLRSAG 83

RESULT 10

ID W40525 standard; Protein; 105 AA.
 AC W40525;
 DT 15-JUL-1998 (first entry)
 DE Human MTS1E1-beta protein.
 KW MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
 KW germ-line mutation; familial melanoma locus; MLM; predisposition.
 OS Homo sapiens.
 PN US5739027-A.
 PD 14-APR-1998.
 PF 07-JUN-1995; 487033.
 PR 07-JUN-1995; US-487033.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 98-250421/22.
 DR N-PSDB; V11249.
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
 PT useful for the diagnosis of cancers related to MTS1E1-beta
 PT mutation(s) and their treatment
 PS Claim 1; Fig 12; 72pp; English.
 CC This sequence represents a human multiple tumour suppression protein,

CC MTS1E1-beta. The MTS gene locus is also referred to as the familial
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum.
SQ Sequence 105 AA;

Query Match 53.0%; Score 473; DB 1; Length 105;
Best Local Similarity 73.5%; Pred. No. 3.94e-35;
Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 1 MMGSGARVAELLHGAEPNCADPATLRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 60

Qy 1 MMGNVHVAALLNNGADSNCEDEPTFSRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 60

Db 61 RLPLDLAEELGHRDVARYLRAA 83

Qy 61 RLPLDLAQERGHQDIVRYLSAG 83

RESULT 11

ID R81701 standard; Protein; 148 AA.

AC R81701;

DT 08-MAY-1996 (first entry)

DE Multiple tumour suppressor 1 (MTS1) polypeptide.

KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;

KW predisposition; melanoma; leukaemia; lymphoma; prognosis;

KW pancreas; breast; thyroid.

OS Homo sapiens.

PN W09525813-A1.

PD 28-SEP-1995. U03537.

PR 17-MAR-1995; US-214582.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215087.

PR 18-MAR-1994; US-215086.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI (UTAH) UNIV UTAH RES FOUND.

PI Cannon-Albright LA, Kamb A, Skolnick MH;

DR WPI: 95-344636/44.

DR N-PSDB: T00736.

DE Detecting polymorphism associated with cancer predisposition - also

PT DNA, vectors and host cells e.g. for gene or protein replacement

PT therapy and drug screening

PS Example 8; Pages 92-93; 148pp; English.

CC An individual can be diagnosed as having a predisposition to cancer

CC by detecting an alteration in the wild type multiple tumour

CC suppressor (MTS) gene, using gene probes which hybridise to the MTS1

CC gene ORF T00736 (which encodes R81701) mutant sequences T00749/50.

CC The above assay can also be used in the diagnosis and prognosis of

CC melanoma, lymphoma, leukaemia and pancreas, breast and thyroid

CC cancers, etc.

SQ Sequence 148 AA;

Query Match 53.0%; Score 473; DB 1; Length 148;
Best Local Similarity 73.5%; Pred. No. 3.94e-35;
Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 44 MMGSGARVAELLHGAEPNCADPATLRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 103

Qy 1 MMGNVHVAALLNNGADSNCEDEPTFSRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 60

Db 104 RLPLDLAEELGHRDVARYLRAA 126

Qy 61 RLPLDLAQERGHQDIVRYLSAG 83

RESULT 12

ID R80940 standard; Protein; 148 AA.

AC R80940;

DT 03-MAY-1996 (first entry)

DE Human multiple tumour suppressor polypeptide, MTS1.
KW Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia;
KW astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
KW gene therapy; chronic.
OS Homo sapiens.
PN W09525429-A1.

PD 28-SEP-1995.

PF 17-MAR-1995; U03316.

PR 18-MAR-1994; US-214581.

PR 18-MAR-1994; US-214582.

PR 18-MAR-1994; US-215086.

PR 18-MAR-1994; US-215088.

PR 18-MAR-1994; US-215087.

PR 14-APR-1994; US-227369.

PR 01-JUN-1994; US-251938.

PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;

DR WPI: 95-344401/44.

DR N-PSDB: Q09158.

PT Wild-type multiple tumour suppressor (MTS) gene and mutant sequences

PT - useful in diagnosis, prognosis and therapy of human cancer, e.g.

PT melanoma or leukaemia

PS Claim 5; Page 92-93; 156pp; English.

CC Several multiple tumour suppressor (MTS) polypeptides have been

CC isolated and sequenced. This sequence is the MTS polypeptide MTS1

CC MTS polypeptide-encoding cDNAs and mutants of these are useful for

CC the diagnosis or prognosis of human cancer. Germ-line mutations of

CC MTS cDNAs can be used for diagnosing predisposition to melanoma,

CC leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's

CC lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus,

CC testis, kidney, stomach and rectum. The wild-type gene is useful

CC for gene therapy and MTS polypeptides may also be used for protein

CC replacement therapy. Also the polypeptides or cells contg. an

CC altered MTS gene are useful for screening for potential cancer

CC therapeutics.

SQ Sequence 148 AA;

Query Match 53.0%; Score 473; DB 1; Length 148;

Best Local Similarity 73.5%; Pred. No. 3.94e-35;

Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 44 MMGSGARVAELLHGAEPNCADPATLRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 103

Qy 1 MMGNVHVAALLNNGADSNCEDEPTFSRPVHDAAREGFLDTLVVLRGAGRLDVRDAG 60

Db 104 RLPLDLAEELGHRDVARYLRAA 126

Qy 61 RLPLDLAQERGHQDIVRYLSAG 83

RESULT 13

ID R53401 standard; Protein; 151 AA.

AC R53401;

DT 07-DEC-1994 (first entry)

DE Inhibitor of cyclin dependent kinase 4 (p16INK4).

KW Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia;

KW lymphoma; cell cycle; detection; identification; tumour virus;

KW proliferating cell nuclear antigen; subunit; complex.

OS Homo sapiens.

PN W09409135-A.

PD 28-APR-1994.

PF 18-OCT-1993; U09945.

PR 16-OCT-1992; US-963308.

PR 17-DEC-1992; US-991997.

PA (COLD-) COLD SPRING HARBOR LAB.

PI Beach DH, Xiong Y;

DR WPI: 94-151320/18.

DR N-PSDB: Q63491.

PT Detection of subunit components of cyclin complexes - used for

PT diagnosing transformation of a cell and developing inhibitors and

PT activators, partic for cancer treatment

PS Claim 13; Page 40; 45pp; English.

CC The cell cycle gene implicated most strongly in oncogenesis is the

CC human cyclin D1. It is genetically linked to the bcl-1 oncogene, a
 CC locus activated by translocation to an immunoglobulin gene enhancer
 CC in some B-cell lymphomas and leukemias. D-type cyclin, cyclin
 CC dependent kinase (CDK), PCNA (proliferating cell nuclear antigen) and
 CC p21 (a 21 kDa polypeptide) exist in a quaternary complex that many
 CC combinatorial variations of the components e.g. cyclin D1 or D3 and
 CC CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may
 CC have a subtly different role in the cell cycle or in different cell
 CC types. Cellular transformation by DNA tumour viruses such as SV40
 CC is associated with selective subunit rearrangement of the cyclin D
 CC complexes. In virally transformed cells, CDK4 totally dissociates
 CC from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton
 CC polypeptide (p16). This sequence, designated p16INK4, binds to and
 CC inhibits CDK4. p16INK4 was discovered to show many similarities to
 CC p16. Reagents, such as monoclonal antibodies, can be developed that
 CC recognise the interactions between the CDK's cyclins, PCNA and low
 CC molecular weight polypeptides and can therefore be used to identify
 CC the state of transformation of a cell.
 CC Sequence 151 AA;

Query Match 53.0%; Score 473; DB 1; Length 151;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 44 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 103
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60
 Db 104 RLPVDLAELGHRDVARYLRAA 126
 QY 61 RLPLDLAQERGHODIVRYLRSAG 83

RESULT 14
 ID W74549 standard; Protein; 156 AA.
 AC W74549;
 DT 04-DEC-1998 (first entry)
 DE Amino acid sequence of multiple tumour suppressor 1.
 KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
 KW somatic mutation; gene therapy.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PF 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-003316.
 PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR N-PSDB; V53819.

PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
 PT useful as hybridisation probes, primers and recombinant production
 PT of MTS in the diagnosis and treatment of cancers related to MTS
 PT mutation(s)
 PS Disclosure: Column 63-64; 73pp; English.
 CC This is the amino acid sequence of the multiple tumour suppressor 1
 CC (MTS-1) protein, used in the method of the invention. The MTS gene
 CC is useful in the diagnosis and prognosis of human cancer, e.g. by
 CC standard nucleic hybridisation techniques, of patient samples. The
 CC mutated sequences are those that are present in somatic mutations
 CC of the gene in cancers. The vectors can be used for gene therapy
 CC strategies to replace function of mutated protein in patients. These
 CC can also be used to construct protein mimetics, also for therapeutic
 CC strategies. In addition the expression constructs can also be used
 CC for recombinant production of MTS. Recombinant MTS can be used to
 CC screen for drugs to be used for cancer therapy, and the protein
 CC itself may also be used to restore MTS function in a cell.
 CC Sequence 156 AA;

Search completed: Thu Jul 20 08:41:38 2000
 Job time : 9 secs.

Query Match 53.0%; Score 473; DB 1; Length 156;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
 Db 52 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 111
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60
 Db 112 RLPVDLAELGHRDVARYLRAA 134
 QY 61 RLPLDLAQERGHODIVRYLRSAG 83

RESULT 15
 ID R85116 standard; Protein; 156 AA.
 AC R85116;
 DT 01-MAR-1996 (first entry)
 DE Cell-cycle regulatory protein p16.
 KW Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
 KW CCR; cancer; cell proliferation.
 OS Homo sapiens.
 PN WQ9528483-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U046336.
 PR 14-APR-1994; US-227371.
 PR 25-MAY-1994; US-248812.
 PR 14-SEP-1994; US-306511.
 PR 29-NOV-1994; US-346147.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
 DR N-PSDB; T02962.

PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.
 PS Claim 1; Page 76-77; 109pp; English.
 CC The human cell-cycle regulatory (CCR) protein p16 (R85116) was
 CC obtd. by expression of a cDNA clone (T02962) isolated in a 2-hybrid
 CC screening assay. CCR p16 specifically inhibits the activity of
 CC cyclin-dependent kinases during various stages of the cell cycle,
 CC and can be used in the treatment and diagnosis of proliferative
 CC disorders.
 CC Sequence 156 AA;

Query Match 53.0%; Score 473; DB 1; Length 156;
 Best Local Similarity 73.5%; Pred. No. 3.94e-35;
 Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 52 MMGSGARVAELLLHGAEPNCADPATLTPRVHDAAREGFDTLVVLRAGARLDVRDANG 111
 QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFDTLVVLRHSGARLDVRDANG 60
 Db 112 RLPVDLAELGHRDVARYLRAA 134
 QY 61 RLPLDLAQERGHODIVRYLRSAG 83

W P S R E L H (TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:43:29 2000; MasPar time 5.20 Seconds

Tabular output not generated. 347.144 Million cell updates/sec

Title: >US-09-016-869A-6
Description: (1-125) from US09016869A.pap
Perfect Score: 892
Sequence: 1 MMGNVHVALLNLGADSN.....SFSSSTPRAELRGSGEQS 125

Scoring table: PAM 150
Gap 11

Searched: 145341 seqs, 14437480 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 28.127; Variance 120.872; scale 0.233

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Length	ID	Description	Pred. No.
1	892 100.0	125	4	PCT-US95-0 Sequence 6, Applicatio	2.41e-75
2	892 100.0	125	2	US-08-306- Sequence 6, Applicatio	2.41e-75
3	892 100.0	125	2	US-08-893- Sequence 6, Applicatio	2.41e-75
4	892 100.0	125	2	US-08-954- Sequence 5, Applicatio	2.41e-75
5	892 100.0	125	3	US-08-581- Sequence 6, Applicatio	2.41e-75
6	892 100.0	125	1	US-08-534- Sequence 5, Applicatio	2.41e-75
7	892 100.0	167	2	US-08-627- Sequence 6, Applicatio	2.41e-75
8	892 100.0	168	2	US-08-508- Sequence 14, Applicati	9.07e-59
9	723 81.1	127	3	US-08-581- Sequence 39, Applicati	7.98e-49
10	621 69.6	85	3	US-08-581- Sequence 38, Applicati	1.62e-34
11	473 53.0	88	3	US-08-581- Sequence 37, Applicati	1.62e-34
12	473 53.0	89	3	US-08-581- Sequence 14, Applicati	1.62e-34
13	473 53.0	105	3	US-09-120- Sequence 14, Applicati	1.62e-34
14	473 53.0	105	2	US-08-486- Sequence 14, Applicati	1.62e-34
15	473 53.0	105	1	US-08-474- Sequence 14, Applicati	1.62e-34
16	473 53.0	105	2	US-08-508- Sequence 14, Applicati	1.62e-34
17	473 53.0	105	1	US-08-480- Sequence 14, Applicati	1.62e-34
18	473 53.0	105	2	US-08-848- Sequence 14, Applicati	1.62e-34
19	473 53.0	105	1	US-08-487- Sequence 14, Applicati	1.62e-34
20	473 53.0	148	4	PCT-US93-0 Sequence 4, Applicatio	1.62e-34
21	473 53.0	148	1	US-08-154- Sequence 4, Applicatio	1.62e-34
22	473 53.0	148	3	US-08-384- Sequence 16, Applicati	1.62e-34
23	473 53.0	148	3	US-08-384- Sequence 24, Applicati	1.62e-34

24	473	53.0	156	4	PCT-US95-0	Sequence 2, Applicatio	1.62e-34
25	473	53.0	156	3	US-08-581-	Sequence 2, Applicatio	1.62e-34
26	473	53.0	156	3	US-09-120-	Sequence 2, Applicatio	1.62e-34
27	473	53.0	156	2	US-08-627-	Sequence 2, Applicatio	1.62e-34
28	473	53.0	156	2	US-08-306-	Sequence 2, Applicatio	1.62e-34
29	473	53.0	156	2	US-08-486-	Sequence 2, Applicatio	1.62e-34
30	473	53.0	156	2	US-08-508-	Sequence 2, Applicatio	1.62e-34
31	473	53.0	156	1	US-08-474-	Sequence 2, Applicatio	1.62e-34
32	473	53.0	156	2	US-08-848-	Sequence 2, Applicatio	1.62e-34
33	473	53.0	156	1	US-08-480-	Sequence 2, Applicatio	1.62e-34
34	473	53.0	156	2	US-08-893-	Sequence 2, Applicatio	1.62e-34
35	473	53.0	156	1	US-08-487-	Sequence 2, Applicatio	1.62e-34
36	473	53.0	391	1	US-08-589-	Sequence 2, Applicatio	1.62e-34
37	472	52.9	136	4	PCT-US96-0	Sequence 6, Applicatio	2.02e-34
38	472	52.9	137	2	US-08-306-	Sequence 4, Applicatio	2.02e-34
39	472	52.9	137	2	US-08-893-	Sequence 4, Applicatio	2.02e-34
40	472	52.9	138	4	PCT-US95-0	Sequence 16, Applicati	2.02e-34
41	472	52.9	138	1	US-08-480-	Sequence 16, Applicati	2.02e-34
42	472	52.9	138	3	US-09-120-	Sequence 16, Applicati	2.02e-34
43	472	52.9	138	1	US-08-474-	Sequence 16, Applicati	2.02e-34
44	472	52.9	138	2	US-08-627-	Sequence 4, Applicatio	2.02e-34
45	472	52.9	138	1	US-08-487-	Sequence 16, Applicati	2.02e-34

ALIGNMENTS

RESULT 1
ID PCT-US95-04636-6 STANDARD; PRT; 125 AA.
XX
AC xxxxxx
XX
DT

Sequence 6, Application PC/TUS9504636

Sequence 6, Application PC/TUS9504636

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

TITLE OF INVENTION: Related Thereto

NUMBER OF SEQUENCES: 10

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Ascii(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04636

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/346,147

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/306,511

FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,812

FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,371

FILING DATE: 14-APR-1994

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 125 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 4; Length 125;

Best Local Similarity 100.0%; Pred. No. 2.41e-75;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC REFERENCE/DOCKET NUMBER: MIV-071.06
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 832-1299
CC TELEFAX: (617) 832-7000
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 125 AA; 13458 MW; 73768 CN;

Query Match 100.0%; Score 892; DB 3; Length 125;
Best Local Similarity 100.0%; Pred. No. 2,41e-75;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNTGADSNCEPTTFSPVHDAAREGFDTLVVLHGSGARLDVWDWG 60
QY 1 MMGNVHVAALLNTGADSNCEPTTFSPVHDAAREGFDTLVVLHGSGARLDVWDWG 60
Db 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
QY 61 RLPLDLAQRGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120

Db 121 SEQES 125
QY 121 SEQES 125

RESULT 6
ID US-08-534-975-5 STANDARD; PRT; 125 AA.

XX xxxxxx

Sequence 5, Application US/08534975

Sequence 5, Application US/08534975

Patent No. 5723313

GENERAL INFORMATION:

APPLICANT: Sherr, Charles, J.

APPLICANT: Quelle, Dawn, E.

TITLE OF INVENTION: ANF-p19, A No. 5723313el Regulator of the Mammalian Cell

TITLE OF INVENTION: Cycle

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,975

FILING DATE: 28-SEP-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Fox, Samuel, L.

REGISTRATION NUMBER: 30,353

REFERENCE/DOCKET NUMBER: 0656.0590000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 125 amino acids

TYPE: amino acid

CC

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Db	43	MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG	10
Qy	1	MMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG	60
Db	103	RLPLDLAQRGHODIVRYLSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTPRALELRGO	162
Qy	61	RLPLDLAQRGHODIVRYLSAGCSLCSAGWSLCTAGNVAQTGDGHSFSSSTPRALELRGO	120
Db	163	SQEQS 167 	
Qy	121	SQEQS 125 	
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ID	US-08-508-735-46	STANDARD;	PRT; 168 AA.
AC	xxxxxx		
XX			
CC	Sequence 46, Application US/08508735		
CC	Sequence 46, Application US/08508735		
CC	Patent No. 5843756		
CC	GENERAL INFORMATION:		
CC	APPLICANT: Stone, Steven		
CC	APPLICANT: Jiang, Ping		
CC	APPLICANT: Kamb, Alexander		
CC	TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF		
CC	NUMBER OF SEQUENCES: 47		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP		
CC	STREET: 1201 New York Avenue, Suite 1000		
CC	CITY: Washington		
CC	STATE: DC		
CC	COUNTRY: USA		
CC	ZIP: 20005		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: Floppy disk		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/508,735		
CC	FILING DATE:		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: US to be assigned		
CC	FILING DATE: 07-JUN-1995		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: PCT/US95/03316		
CC	FILING DATE: 17-MAR-1995		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: Ihnen, Jeffrey L.		
CC	REGISTRATION NUMBER: 28,957		
CC	REFERENCE/DOCKET NUMBER: 24884-109348		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: 202-962-4848		
CC	TELEFAX: 202-962-8300		
CC	INFORMATION FOR SEQ ID NO: 46:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 168 amino acids		
CC	TYPE: amino acid		
CC	STRANDEDNESS: single		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	HYPOTHETICAL: NO		
CC	ORIGINAL SOURCE:		
CC	ORGANISM: Mus musculus		
CC	SEQUENCE 168 AA; 17901 MW; 133219 CN;		
SO			

CC NAME: Vincent, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: MIV-071.06
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 832-1299
CC TELEFAX: (617) 832-7000
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 127 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal
CC SEQUENCE 127 AA: 13611 MW: 89090 CN;
SQ

Query Match 81.1%; Score 723; DB 3; Length 127;
Best Local Similarity 81.1%; Pred. No. 9,07e-59;
Matches 103; Conservative 0; Mismatches 22; Indels 2; Gaps 2;

Db 1 MMGXVAXLLXGXGKNCXDPXTXXXRPVHDAAREGFLDTLVVHXGARGLDVDRDAW 60
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVVHSGARGLDVDRDAW 59
Db 61 GRPLDIAEXGHDXHXVYLRXAGXGSLCSAGWSLCTAGNVAQTGCHFSSTPRALRLR 120
QY 60 GRPLDIAQERGHQDIVRYLRSAG-CCSLCSAGWSLCTAGNVAQTGCHFSSTPRALRLR 118
Db 121 GOSQEOS 127
QY 119 GOSQEOS 125

RESULT 10
ID US-08-581-918A-39 STANDARD; PRT; 85 AA.
XX
AC XXXXXX
DT
XX
XX
XX
DE Sequence 39, Application US/08581918A
CC Sequence 39, Application US/08581918A
CC Patent No. 6043030
CC GENERAL INFORMATION:
CC APPLICANT: Beach, David H.
CC APPLICANT: Demetrick, Douglas J.
CC APPLICANT: Serrano, Manuel
CC APPLICANT: Hannon, Gregory J.
CC TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
CC NUMBER OF SEQUENCES: 39
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley, Hoag & Eliot
CC STREET: One Post Office Square
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Wordpad
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/581,918A
CC FILING DATE: 02-JAN-1996
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/497,214
CC FILING DATE: 30-JUN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/346,147

CC FILING DATE: 29-NOV-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/306,511
CC FILING DATE: 14-SEP-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/248,812
CC FILING DATE: 25-MAY-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/227,371
CC FILING DATE: 14-APR-1994
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/154,915
CC FILING DATE: 18-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/991,997
CC FILING DATE: 17-DEC-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Vincent, Matthew P.
CC REGISTRATION NUMBER: 36,709
CC REFERENCE/DOCKET NUMBER: MIV-071.06
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (617) 832-1299
CC TELEFAX: (617) 832-7000
CC INFORMATION FOR SEQ ID NO: 39:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 85 amino acids
CC TYPE: amino acid
CC STRANDEDNESS:
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 85 AA: 9307 MW: 32299 CN;
SQ

Query Match 69.6%; Score 621; DB 3; Length 85;
Best Local Similarity 100.0%; Pred. No. 7.98e-49;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVVHSGARGLDVDRDAW 60
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLVVHSGARGLDVDRDAW 60
Db 61 RLPLDLAQERGHQDIVRYLRSAGCS 85
QY 61 RLPLDLAQERGHQDIVRYLRSAGCS 85

RESULT 11
ID US-08-581-918A-38 STANDARD; PRT; 88 AA.
XX
AC XXXXXX
DT
XX
XX
DE Sequence 38, Application US/08581918A
CC Sequence 38, Application US/08581918A
CC Patent No. 6043030
CC GENERAL INFORMATION:
CC APPLICANT: Beach, David H.
CC APPLICANT: Demetrick, Douglas J.
CC APPLICANT: Serrano, Manuel
CC APPLICANT: Hannon, Gregory J.
CC TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
CC NUMBER OF SEQUENCES: 39
CC NUMBER OF SEQUENCES: 39
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley, Hoag & Eliot
CC STREET: One Post Office Square
CC CITY: Boston
CC STATE: MA
CC COUNTRY: USA
CC ZIP: 02109
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

M P Q S R E L E H

(TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:41:56 2000; MasPar time 10.59 Seconds
556.609 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-6
Description: (1-125) from US09016869A.pep
Perfect Score: 892
Sequence: 1 MMGNVHVAALLNYGADSN.....SFSSSTPRALELRGQSQEQS 125

Scoring table: PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir63
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 41.141; Variance 75.478; scale 0.545

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	892	100.0		167	2	158352	pl6INK4a - mouse	2.02e-169
2	473	53.0		156	2	JE0141	cyclin dependent kina	4.04e-76
3	472	52.9		138	2	B55479	CDK4 inhibitor p14(IN	6.66e-76
4	461	51.7		130	2	178845	pl5INK4b - mouse	1.62e-73
5	233	26.1		164	2	A53738	cyclin-dependent kina	7.47e-26
6	228	25.6		41	2	152720	gene pl5INK4B protein	7.19e-25
7	218	24.4		166	2	B57378	cyclin-dependent kina	6.47e-23
8	218	24.4		166	2	A53739	CDK4/CDK6 inhibitor p	6.47e-23
9	198	22.2		168	2	B57379	CDK4/CDK6 inhibitor p	4.56e-19
10	193	21.6		168	2	A55478	CDK6 inhibitor p18 -	4.05e-18
11	156	17.5		2531	2	S18198	notch protein homolog	2.58e-11
12	154	17.3		2555	2	A40043	notch protein homolog	5.86e-11
13	149	16.7		2531	2	A46019	Notch-1 protein - mou	4.46e-10
14	148	16.6		638	2	A56695	notch2 protein homolo	6.67e-10
15	148	16.6		2471	2	A49128	cell-fate determining	6.67e-10
16	147	16.5		2318	2	S45306	notch 3 protein - mou	9.97e-10
17	147	16.5		2321	2	S78549	notch3 protein - huma	9.97e-10
18	146	16.4		2437	2	S42612	transmembrane protein	1.49e-09
19	140	15.7		3924	2	S37431	ankyrin 2, neuronal 1	1.62e-08
20	138	15.5		1423	1	137275	death-associated prot	3.56e-08
21	138	15.5		2524	2	A35844	Xotch protein - Afri	3.56e-08
22	136	15.2		1848	2	S37711	ankyrin, erythrocyte	7.79e-08
23	136	15.2		1856	2	B35049	ankyrin 1, erythrocyt	7.79e-08

24	136	15.2	1862	2	149502	ankyrin - mouse	7.79e-08
25	136	15.2	1880	2	A35849	ankyrin 1, erythrocyt	7.79e-08
26	136	15.2	1881	1	SJHUK	ankyrin 1, erythrocyt	7.79e-08
27	133	14.9	1549	2	T13940	ankyrin - fruit fly (2.50e-07
28	131	14.7	1411	2	S30355	alpha-latroinsectotox	5.41e-07
29	130	14.6	4377	2	A55575	ankyrin 3, long splic	7.94e-07
30	129	14.5	1786	2	A57282	ankyrin-related prote	1.16e-06
31	129	14.5	1809	2	T15345	ankyrin-related unc-4	1.16e-06
32	129	14.5	1815	2	T15346	elegans ankyrin-relat	1.16e-06
33	129	14.5	1867	2	T15344	ankyrin-related unc-4	1.16e-06
34	129	14.5	2039	2	T15347	ankyrin-related unc-4	1.16e-06
35	124	13.9	209	2	T15888	hypothetical protein	7.74e-06
36	120	13.5	1401	2	S11527	alpha-latrotoxin prec	3.44e-05
37	119	13.3	2703	1	A24420	notch protein - fruit	4.98e-05
38	116	13.0	334	2	T09017	probable acyl-CoA bin	1.50e-04
39	115	12.9	934	1	H71274	probable ankyrin - sy	2.15e-04
40	109	12.2	323	2	B47169	ankyrin-like repeat p	1.85e-03
41	109	12.2	482	2	B44368	cactus - fruit fly (D	1.85e-03
42	109	12.2	500	2	A44368	cactus - fruit fly (D	1.85e-03
43	109	12.2	500	2	A44369	ankyrin repeat acidic	1.85e-03
44	108	12.1	201	2	F64758	yand protein - Escher	2.63e-03
45	105	11.8	1436	2	S57238	forked protein 5.4K -	7.49e-03

ALIGNMENTS

RESULT 1
ENTRY I58352 #type complete
TITLE pl6INK4a - mouse
ORGANISM #formal_name Mus sp. #common_name mouse
DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 28-Feb-1997

ACCESSIONS I58352
REFERENCE I58352
#authors Queller, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; Walker, C.; Beach, D.; Sherr, C.J.; Serrano, M.

#journal Oncogene (1995) 11:635-645
#title Cloning and characterization of murine pl6INK4a and pl5INK4b genes.

#cross-references MUID:95380169
#accession I58352
#status preliminary; translated from GB/EMBL/DDBJ
#molecule_type mRNA
##residues 1-167 #label RES
##cross-references GB:S79251; NID:g1087090; PID:g1087091

GENETICS
#gene pl6INK4a
SUMMARY #length 167 #molecular-weight 17870 #checksum 1257

Query Match 100.0%; Score 892; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.02e-169;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVDRDAG 102
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVDRDAG 60
|||||

Db 103 RLPLDLAQERGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTPRALELRGQ 162
QY 61 RLPLDLAQERGHQDIVYRLSAGCSLCSAGWSLCTAGNVAQTGHSFSSSTPRALELRGQ 120
|||||

Db 163 SQEQS 167
QY 121 SQEQS 125
|||||

RESULT 2
ENTRY JE0141 #type complete
TITLE cyclin dependent kinase - human
ALTERNATE_NAMES CDK4 inhibitor pl6INK4a/MTS1; cyclin-dependent kinase inhibitor 2A; multiple tumor suppressor 1 (MTS1)
ORGANISM #formal_name Homo sapiens #common_name man

SUMMARY	length 164	molecular-weight 17362	#checks 5271
Query Match	26.1%	Score 233;	DB 2; Length 164;
Best Local Similarity	46.5%	Pred. No. 7.47e-26;	
Matches	40; Conservative	15; Mismatches	29; Indels 2; Gaps 2;
Db	48 MMFGSTALELLKQAGSPNVQDTSG-TSPVHDAARTGFLDTLKVLVEGADVNVDGTG	106	
QY	1 MMGMNVHVAALLNGAGDSNCEPTTFSPRPVHDAAREGFLDTLVLHGSGARLDVRDAGW	60	
Db	107 ALPIHLAVQEGHTAVVSEL-AAESDL	131	
QY	61 RLPLDLAQERGHQDIVRLRSAGCSL	86	
RESULT	6		
ENTRY	I52720	#type fragment	
TITLE	gene p15INK4B protein - rat (fragment)		
ORGANISM	#formal_name Rattus sp. #common_name rat		
DATE	26-Jul-1996 #sequence_revision 26-Jul-1996	#text_change	
ACCESSIONS	28-Feb-1997		
REFERENCE	I52720		
#authors	Knapke, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.		
#journal	Cancer Res. (1995) 55:1607-1612		
#title	Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.		
#cross-references	MUID:95228036		
#accession	I52720		
#status	preliminary; translated from GB/EMBL/DBJ		
#molecule_type	DNA		
#residues	1-41 #label RES		
#cross-references	GB:S77734; NID:g998711		
GENETICS			
#gene	p15INK4B		
SUMMARY	length 41	#checks 3296	
Query Match	25.6%	Score 228; DB 2; Length 41;	
Best Local Similarity	70.7%	Pred. No. 7.19e-25;	
Matches	29; Conservative	7; Mismatches	5; Indels 0; Gaps 0;
Db	1 MMGSAQVAEALLLHGAPNCADPATLTPVHDAAREGFLD	41	
QY	1 MMGMNVHVAALLNGAGDSNCEPTTFSPRPVHDAAREGFLD	41	
RESULT	7		
ENTRY	B57378	#type complete	
TITLE	cyclin-dependent kinase inhibitor p19 - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	08-Feb-1996 #sequence_revision 08-Feb-1996	#text_change	
ACCESSIONS	20-Sep-1999		
REFERENCE	B57378		
#authors	Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.		
#journal	Mol. Cell. Biol. (1995) 15:2682-2688		
#title	Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16(ink4).		
#cross-references	MUID:95257949		
#accession	B57378		
#status	preliminary		
#molecule_type	mRNA		
#residues	1-166 #label CHA		
#cross-references	GB:020497; NID:g791204; PID:AA85437.1; PID:g791205		
CLASSIFICATION	#superfamily unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology		
SUMMARY	length 166	#molecular-weight 17920	#checks 3767
Query Match	24.4%	Score 218; DB 2; Length 166;	
Best Local Similarity	48.1%	Pred. No. 6.47e-23;	
Matches	38; Conservative	13; Mismatches	27; Indels 1; Gaps 1;

development.
#cross-references MUID:92111383
#accession S18188
#molecule_type mRNA
#residues 1-2531 #label WEI
#cross-references EMBL:X57405; NID:g57634; PID:g57635
CLASSIFICATION superfamily unassigned ankyrin repeat proteins; ankyrin repeat homology; Egf homology

```

FEATURE
  987-1018      #domain EGF homology #label EGF1\
  1025-1056      #domain EGF homology #label EGF\
  1233-1264      #domain EGF homology #label EGF2\
  1917-1949      #domain ankyrin repeat homology #label AN1\
  1950-1982      #domain ankyrin repeat homology #label AN2\
  1984-2016      #domain ankyrin repeat homology #label AN3\
  2017-2049      #domain ankyrin repeat homology #label AN4\
  2050-2082      #domain ankyrin repeat homology #label AN5\
SUMMARY
  Query Match          17.58; Score 156; DB 2; Length 2531;
  Best Local Similarity 42.98; Pred.No. 2.58e-11;
  Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2028 VNVVDAVLLKNGANKDMONNKE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2086
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 3  MGNVHVAALLNNGADSNCEDPPTFSRPVHDAAREGFLDTLVVLHSGSARLDVVDAGRL 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 2087 PRDIAQERMHHDIVRL 2103
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 12
ENTRY      A40043      #type complete
TITLE      notch protein homolog TAN-1 precursor - human
ORGANISM   Homo sapiens #common_name man
DATE       21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change
           13-Aug-1999
ACCESSIONS A40043
REFERENCE   Ellis, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds,
            T.C.; Smith, S.D.; Sklar, J.
            Cell (1991) 66:649-661
            TAN-1, the human homolog of the Drosophila Notch gene, is
            broken by chromosomal translocations in T lymphoblastic
            neoplasms.
#cross-references MUID:91347367
#accession      A40043
#status          preliminary; nucleic acid sequence not shown; not
                compared with conceptual translation
#molecule_type mRNA
#residues        1-2555 #label ELL
#cross-references GB:M73980
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
                repeat homology; EGF homology
FEATURE
  261-292      #domain EGF homology #label EGY1\
  494-525      #domain EGF homology #label EGF1\
  987-1018      #domain EGF homology #label EGF2\
  1149-1180      #domain EGF homology #label EGF2\
  1187-1218      #domain EGF homology #label EGF3\
  1233-1264      #domain EGF homology #label EGF3\
  1927-1959      #domain ankyrin repeat homology #label AN1\
  1960-1992      #domain ankyrin repeat homology #label AN2\
  1994-2026      #domain ankyrin repeat homology #label AN3\
  2027-2059      #domain ankyrin repeat homology #label AN4\
  2060-2092      #domain ankyrin repeat homology #label AN5\
SUMMARY
  Query Match          17.38; Score 154; DB 2; Length 2555;
  Best Local Similarity 42.98; Pred.No. 5.8e-11;
  Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2038 VNVVDAVLLKNGANKDMONNKE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2096
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 3  MGNVHVAALLNNGADSNCEDPPTFSRPVHDAAREGFLDTLVVLHSGSARLDVVDAGRL 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 2097 PRDIAQERMHHDIVRL 2113
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 PLDLAQERGHQDIVRYL 79

```

```

RESULT 13
ENTRY      A46019      #type complete
TITLE      Notch-1 protein - mouse
ALTERNATE_NAMES
  #formal_name Mus musculus #common_name house mouse
  #formal_name Mus musculus #common_name house mouse
DATE       22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
           20-Sep-1999
ACCESSIONS A46019; S25144
REFERENCE   del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins,
            N.A.; Copeland, N.G.; Gridley, T.
            Genomics (1993) 15:259-264
            Cloning, analysis, and chromosomal localization of Notch-1, a
            mouse homolog of Drosophila Notch.
#cross-references MUID:93194170
#accession      A46019
#status          not compared with conceptual translation
#molecule_type nucleic acid
#residues        1-2531 #label DEL
#cross-references GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
           PID:g288503
#note           sequence extracted from NCBI backbone (NCBIP:127318)
REFERENCE      S25144
            Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.;
            Gendron-Maguire, M.; Greenspan, R.J.; McMahon, A.P.;
            Gridley, T.
            submitted to the EMBL Data Library, April 1992
            Expression pattern of Notch, a mouse homolog of Drosophila
            Notch, suggests an important role in early postimplantation
            mouse development.
#accession      S25144
#molecule_type mRNA
#residues        1551-2108, 'Q', '2110-2114', 'ALP', 2118-2170 #label FRA
#cross-references EMBL:Z11886
GENETICS
#gene           notch-1
#map_position    2
#note           proximal region of chromosome 2
#superfamily unassigned ankyrin repeat proteins; ankyrin
            repeat homology; EGF homology
CLASSIFICATION
FEATURE
  106-138      #domain EGF homology #label EGF1\
  144-175      #domain EGF homology #label EGF1\
  222-254      #domain EGF homology #label EGF2\
  261-292      #domain EGF homology #label EGF2\
  339-370      #domain EGF homology #label EGF3\
  416-449      #domain EGF homology #label EGF3\
  456-487      #domain EGF homology #label EGF3\
  494-525      #domain EGF homology #label EGF5\
  532-563      #domain EGF homology #label EGF6\
  607-638      #domain EGF homology #label EGF7\
  682-713      #domain EGF homology #label EGF8\
  757-788      #domain EGF homology #label EGF9\
  795-826      #domain EGF homology #label EGF10\
  873-904      #domain EGF homology #label EGF11\
  911-942      #domain EGF homology #label EGF12\
  949-980      #domain EGF homology #label EGF13\
  987-1018      #domain EGF homology #label EGF14\
  1025-1056      #domain EGF homology #label EGF15\
  1063-1094      #domain EGF homology #label EGF16\
  1149-1180      #domain EGF homology #label EGF17\
  1187-1218      #domain EGF homology #label EGF18\
  1233-1264      #domain EGF homology #label EGF18\
  1352-1383      #domain EGF homology #label EGF19\
  1391-1425      #domain ankyrin repeat homology #label AN1\
  1917-1948      #domain ankyrin repeat homology #label AN2\
  1949-1981      #domain ankyrin repeat homology #label AN3\
  1983-2015      #domain ankyrin repeat homology #label AN4\
  2016-2048      #domain ankyrin repeat homology #label AN5\
  2049-2081      #domain ankyrin repeat homology #label AN5\
SUMMARY
  #length 2531 #molecular-weight 271312 #checksum 6611

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Query Match      16.78; Score 149; DB 2; Length 2531;
Best Local Similarity 37.78; Pred. No. 4.46e-10;
Matches 29; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

Db 2027 VNNYDAAVLLKNGKANDIENKEETSLFSLIRRESYETAKVLLDHFANR-DITDHMDRL 2085
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDANGRL 62

Db 2086 PRDIAQRMHHDIVRL 2102
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 14
ENTRY      A56695      #type fragment
TITLE      notch2 protein homolog - human (fragment)
ALTERNATE_NAMES notch hn
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change
ACCESSIONS A56695; G02458
REFERENCE   Stifani, S.; Blaumueller, C.M.; Redhead, N.J.; Hill, R.E.;
            Artavanis-Tsakonas, S.
#journal   Nature Genet. (1992) 2:119-127
#title     Human homologs of a Drosophila enhancer of split gene product
            Define a novel family of nuclear proteins.
#cross-references MUID:93265135
#accession A56695
#status    preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues  1-638 #label STI
#cross-references GB:M99437; NID:g189263; PIDN:AAA36377.1; PID:g189264
REFERENCE   H01314
#authors   Fisher, E.M.C.
#submission submitted to the EMBL Data Library, March 1996
#accession G02458
#status    preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues  157-221 #label FIS
#cross-references EMBL:U50549; NID:g1293642; PIDN:AAB17664.1;
            PID:g1293643
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
            repeat homology; EGF homology
            tandem repeat; transmembrane protein
KEYWORDS
FEATURE
69-101      #domain ankyrin repeat homology #label AN1\
102-134      #domain ankyrin repeat homology #label AN2\
136-168      #domain ankyrin repeat homology #label AN3\
169-201      #domain ankyrin repeat homology #label AN4\
202-234      #domain ankyrin repeat homology #label AN5\
SUMMARY      #length 638 #checksum 7438

Query Match      16.68; Score 148; DB 2; Length 638;
Best Local Similarity 39.08; Pred. No. 6.67e-10;
Matches 30; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

Db 180 VNNVEATLLKNGKANDMDQNK-EPTPLFAAREGSYEAAILLDHFANRDTDHMDRL 238
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDANGRL 62

Db 239 PRDVARDRMHHDIVRL 255
QY 63 PLDLAQERGHQDIVRYL 79

RESULT 15
ENTRY      A49128      #type complete
TITLE      cell-fate determining gene Notch2 protein - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
            13-Aug-1999
ACCESSIONS A49128
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REFERENCE
#authors     Weinmaster, G.; Roberts, V.J.; Lemke, G.
#journal     Development (1992) 116:931-941
#title       Notch2: a second mammalian Notch gene.
#cross-references MUID:93202015
#accession   A49128
#status      preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues    1-2471 #label WEI
#experimental_source Schwann cell
#note        #sequence extracted from NCBI backbone (NCBIP:127811)
            #superfamily unassigned ankyrin repeat proteins; ankyrin
            repeat homology; EGF homology
CLASSIFICATION
FEATURE
264-295      #domain EGF homology #label EGX1\
799-830      #domain EGF homology #label EGX1\
877-908      #domain EGF homology #label EGX2\
1029-1060     #domain EGF homology #label EGX\
1067-1098     #domain EGF homology #label EGX3\
1153-1184     #domain EGF homology #label EGX3\
1191-1222     #domain EGF homology #label EGX4\
1376-1908     #domain ankyrin repeat homology #label AN1\
1376-1908     #domain ankyrin repeat homology #label AN2\
1376-1908     #domain ankyrin repeat homology #label AN3\
1376-1908     #domain ankyrin repeat homology #label AN4\
1376-1908     #domain ankyrin repeat homology #label AN5\
2009-2041     #length 2471 #molecular-weight 265367 #checksum 5929
SUMMARY
Query Match      16.6%; Score 148; DB 2; Length 2471;
Best Local Similarity 39.0%; Pred. No. 6.67e-10;
Matches 30; Conservative 15; Mismatches 31; Indels 1; Gaps 1;

Db 1987 VNNVEATLLKNGKANDMDQNK-EPTPLFAAREGSYEAAILLDHFANRDTDHMDRL 2045
QY 3 MGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVYRDANGRL 62

Db 2046 PRDVARDRMHHDIVRL 2062
QY 63 PLDLAQERGHQDIVRYL 79

Search completed: Thu Jul 20 08:42:09 2000
JOB time : 13 secs.
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FT VARSPLIC 1 42 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 167 AA; 17870 MW; 88C4588A105ECB8F CRC64;

Query Match 100.0%; Score 892; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.00e-191;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 MMGMNVHVAALLNGADSNCEPDTTFRPVDHAAAREGFLDTLVVHGSGARLVDRAWG 102
|||||
QY 1 MMGMNVHVAALLNGADSNCEPDTTFRPVDHAAAREGFLDTLVVHGSGARLVDRAWG 60
|||||

Db 103 RLPLDLAQRGHODIVYRLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSPRALELRGQ 162
|||||
QY 61 RLPLDLAQRGHODIVYRLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSPRALELRGQ 120
|||||

Db 163 SQEQS 167
|||||
QY 121 SQEQS 125
|||||

RESULT 2
ID CDKN2 HUMAN STANDARD; PRT; 156 AA.
AC P42771; Q15191;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)
DE (MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).
GN CDKN2A OR CDKN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94081956.
RA Serrano M., Hannon G.J., Beach D.;
RT "A new regulatory motif in cell-cycle control causing specific
RT inhibition of cyclin D/CDK4.";
RL Nature 366:704-707(1993).
RN [2]
RP SEQUENCE OF 51-152 FROM N.A.
RX MEDLINE; 94204645.
RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
RA Skolnick M.H.;
RT "A cell cycle regulator potentially involved in genesis of many tumor
RT types.";
RL Science 264:436-440(1994).
RN [3]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE; 96182088.
RA Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;
RT "Regulation of p16CDKN2 expression and its implications for cell
RT immortalization and senescence.";
RL Mol. Cell. Biol. 16:859-867(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
RX MEDLINE; 98421670.
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
RT by the tumour suppressor p16INK4a.";
RL Nature 395:237-243(1998).
RN [5]
RP REVIEW ON MELANOMA VARIANTS.
RX MEDLINE; 96377761.
RA Dracopoli N.C., Fountain J.W.;
RT "CDKN2 mutations in melanoma.";
RL Cancer Surv. 26:115-132(1996).
RN [6]
RP REVIEW ON VARIANTS.
RX MEDLINE; 96303699.
RA Smith-Soerensen B., Hovig E.;
RT "CDKN2A (p16INK4A) somatic and germline mutations.";

Hum. Mutat. 7:294-303(1996).
[7]
RN VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
RX MEDLINE; 94338359.
RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK4
RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small
RT cell lung carcinomas.";
RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
RN [8]
RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.
RX MEDLINE; 95078916.
RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,
RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;
RT "Germline p16 mutations in familial melanoma.";
RL Nat. Genet. 8:15-21(1994).
RN [9]
RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
RX MEDLINE; 95060835.
RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
RA Abraham J.M., Meltzer S.J.;
RT "The MTS1 gene is frequently mutated in primary human esophageal
RT tumors.";
RL Oncogene 9:3737-3741(1994).
RN [10]
RP VARIANTS.
RX MEDLINE; 95188190.
RA Okamoto A., Hussian S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in
RT primary and metastatic lung cancer.";
RL Cancer Res. 55:1448-1451(1995).
RN [11]
RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.
RX MEDLINE; 96121580.
RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma
RT kindreds.";
RL Hum. Mol. Genet. 4:1845-1852(1995).
RN [12]
RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.
RX MEDLINE; 95375774.
RA Ranade K., Hussussian C.J., Sikorski R.S., Varnus H.E.,
RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
RA Dracopoli N.C.;
RT "Mutations associated with familial melanoma impair p16INK4
RT function.";
RL Nat. Genet. 10:114-116(1995).
RN [13]
RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.
RX MEDLINE; 96323259.
RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
RA Tselbacher K.J., Sober A.J., Haber D.A.;
RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in
RT familial melanoma: analysis of a clinic-based population.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
RN [14]
RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.
RX MEDLINE; 97472457.
RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,
RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,
RA Bishop D.T., Bishop J.N.;
RT "Germline mutations of the CDKN2 gene in UK melanoma families.";
RL Hum. Mol. Genet. 6:2061-2067(1997).
RN [15]
RP VARIANTS FAMILIAL MELANOMA.
RX MEDLINE; 98087572.
RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombléd J.,
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone

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DR EMBL: S79760; AAB35360.1; -;
DR EMBL: S77734; CAB33639.1; -;
DR PFAM: PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
FT CHAIN 46 130 SHORT FORM.
FT INIT_MET 46 46 FOR THE SHORT FORM.
FT DOMAIN 5 95 2 X ANK MOTIF REPEATS.
FT REPEAT 5 31 ANK MOTIF 1 (INCOMPLETE).
FT REPEAT 65 95 ANK MOTIF 2.
SQ SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match 51.28; Score 457; DB 1; Length 130;
Best Local Similarity 72.08; Pred. No. 2.90e-82;
Matches 59; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

Db 46 MMGSAQVAELLLHGNPCADPAITRPVHDAAREGFLDTLMVLKAGARLDVCDWG 105
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLMVLHSGSARLDVRDAG 60
Db 106 RLPVDAEQQHGRDIARYLHAA 127
QY 61 RLPDLAQERGHQDIVRYLRS 82

RESULT 6
ID CDN2_MONDO STANDARD; PRT; 171 AA.
AC Q77617;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4) (P16-INK4)
DE (TUMOR SUPPRESSOR CDKN2A).
GN CDKN2A.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
RN [1]
RP SEQUENCE FROM N.A.
RA Sherburn T.E., Gale J.M., Lev R.D.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -----
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
CC -----
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DR EMBL: AF064808; AAC23669.1; -;
DR EMBL: AF064808; AAC23670.1; -;
DR PFAM: PF00023; ank; 3.
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
FT DOMAIN 46 169 4 X ANK MOTIF REPEATS.
FT REPEAT 46 77 ANK MOTIF 1 (INCOMPLETE).

FT REPEAT 78 109 ANK MOTIF 2.
FT REPEAT 111 143 ANK MOTIF 3.
FT REPEAT 144 169 ANK MOTIF 4.
FT VARSPLIC 1 34 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;
Query Match 48.78; Score 434; DB 1; Length 171;
Best Local Similarity 71.38; Pred. No. 1.19e-76;
Matches 57; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

Db 86 MMGNVRLAAILLOYGAENPTDPTTLTPVHDAAREGFLDTLMVLHAGARLDVRDSWG 145
QY 1 MMGNVHVAALLNYGADSNCEPTTFSPVHDAAREGFLDTLMVLHSGSARLDVRDAG 60
Db 146 RLPVDAEQQHGHVYVAYLR 165
QY 61 RLPDLAQERGHQDIVRYLR 80

RESULT 7
ID CDN7_HUMAN STANDARD; PRT; 166 AA.
AC P55273; Q13102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NONE MARROW;
RX MEDLINE; 96121373.
RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
RA Lahti J.M., Sherr C.J., Downing J.R.;
RT "Molecular cloning, expression pattern, and chromosomal localization
RT of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases";
RL Genomics 29:632-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96362662.
RA Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
RA Zarwala M., Matera A.G., Xiong Y.;
RT "Isolation and characterization of p19INK4d, a p16-related inhibitor
RT specific to CDK6 and CDK4";
RL Mol. Biol. Cell 7:57-70(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RX MEDLINE; 95257949.
RA Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.;
RT "Identification of human and mouse p19, a novel CDK4 and CDK6
RT inhibitor with homology to p16ink4";
RL Mol. Cell. Biol. 15:2682-2688(1995).
RN [4]
RP SEQUENCE FROM N.A.
RA Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
RA Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
RA Bishop D.T.;
RT "Mutation testing in melanoma families: INK4a, CDK4 and INK4D";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
RX MEDLINE; 98421670.
RA Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
RT "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
RT by the tumour suppressor p16INK4a";
RL Nature 395:237-243(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE; 98455510.
RA Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engn R.A.,

GN NOTCH1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-SCHWANN CELL;
RX MEDLINE; 9211383.
RA Weinmaster G.; Roberts V.J.; Lenke G.;
RT "A homolog of Drosophila Notch expressed during mammalian
RL development."; Development 113:199-205(1991).
RN (2)
RP REVISIONS TO 1652-1653.
RA Weinmaster G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: REQUIRED FOR THE CORRECT DIFFERENTIATION OF A NUMBER
CC OF TISSUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST LEVELS OCCUR BETWEEN
CC DAYS 12 AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE
CC ADULT.
CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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DR EMBL; X57405; CAA40667.1; -;
DR HSP; P00740; IYX.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 26.
DR PROSITE; PS01187; EGF_CA; 21.
DR PFAM; PF00008; EGF; 36.
DR PFAM; PF00023; ank; 6.
DR PFAM; PF00066; notch; 3.
DR KW Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain;
KW Transmembrane; Signal; Glycoprotein.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 2531 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1.
FT DOMAIN 19 1723 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1724 1746 POTENTIAL.
FT DOMAIN 1747 2531 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 58 EGF-LIKE 1.
FT DOMAIN 59 99 EGF-LIKE 2.
FT DOMAIN 102 139 EGF-LIKE 3.
FT DOMAIN 140 176 EGF-LIKE 4.
FT DOMAIN 178 216 EGF-LIKE 5.
FT DOMAIN 218 255 EGF-LIKE 6.
FT DOMAIN 257 293 EGF-LIKE 7.
FT DOMAIN 295 333 EGF-LIKE 8.
FT DOMAIN 335 371 EGF-LIKE 9.
FT DOMAIN 372 410 EGF-LIKE 10.
FT DOMAIN 412 450 EGF-LIKE 11.
FT DOMAIN 452 488 EGF-LIKE 12.
FT DOMAIN 490 526 EGF-LIKE 13.
FT DOMAIN 528 564 EGF-LIKE 14.
FT DOMAIN 566 601 EGF-LIKE 15.
FT DOMAIN 603 639 EGF-LIKE 16.
FT DOMAIN 641 676 EGF-LIKE 17.
FT DOMAIN 678 714 EGF-LIKE 18.
FT DOMAIN 716 751 EGF-LIKE 19.
FT DOMAIN 753 789 EGF-LIKE 20.
FT DOMAIN 791 827 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT 829 867
FT DOMAIN 869 905
FT DOMAIN 907 943
FT DOMAIN 945 981
FT DOMAIN 983 1019
FT DOMAIN 1021 1057
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FT DOMAIN 1097 1143
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FT 591 600


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FT DOMAIN 984 1020 EGF-LIKE 26. BY SIMILARITY.
FT DOMAIN 1022 1058 EGF-LIKE 27. BY SIMILARITY.
FT DOMAIN 1060 1096 EGF-LIKE 28. BY SIMILARITY.
FT DOMAIN 1098 1144 EGF-LIKE 29. BY SIMILARITY.
FT DOMAIN 1146 1182 EGF-LIKE 30. BY SIMILARITY.
FT DOMAIN 1184 1220 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL). BY SIMILARITY.
FT DOMAIN 1222 1266 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL). BY SIMILARITY.
FT DOMAIN 1308 1366 EGF-LIKE 33. BY SIMILARITY.
FT DOMAIN 1368 1404 EGF-LIKE 34. BY SIMILARITY.
FT DOMAIN 1406 1442 EGF-LIKE 35. BY SIMILARITY.
FT DOMAIN 1444 1480 EGF-LIKE 36. BY SIMILARITY.
FT DOMAIN 1482 1518 3 X LIN/NOTCH REPEATS. BY SIMILARITY.
FT DOMAIN 1520 1556 LIN/NOTCH 1. BY SIMILARITY.
FT DOMAIN 1558 1594 LIN/NOTCH 2. BY SIMILARITY.
FT DOMAIN 1596 1632 LIN/NOTCH 3. BY SIMILARITY.
FT DOMAIN 1634 1670 6 X ANK MOTIF REPEATS. BY SIMILARITY.
FT DOMAIN 1672 1708 ANK MOTIF 1. BY SIMILARITY.
FT DOMAIN 1710 1746 ANK MOTIF 2. BY SIMILARITY.
FT DOMAIN 1748 1784 ANK MOTIF 3. BY SIMILARITY.
FT DOMAIN 1786 1822 ANK MOTIF 4. BY SIMILARITY.
FT DOMAIN 1824 1860 ANK MOTIF 5. BY SIMILARITY.
FT DOMAIN 1862 1898 ANK MOTIF 6. BY SIMILARITY.
FT DOMAIN 1900 1936 POLY-VAL. BY SIMILARITY.
FT DOMAIN 1938 1974 POLY-ARG. BY SIMILARITY.
FT DOMAIN 1976 2012 POLY-PRO. BY SIMILARITY.
FT DOMAIN 2014 2050 POLY-ALA. BY SIMILARITY.
FT DOMAIN 2052 2088 POLY-GLU. BY SIMILARITY.
FT DOMAIN 2090 2126 POLY-GLY. BY SIMILARITY.
FT DOMAIN 2128 2164 POLY-GLN. BY SIMILARITY.
FT DOMAIN 2166 2202 POLY-PRO. BY SIMILARITY.
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FT DOMAIN 5662 5698 BY SIMILARITY.
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FT DOMAIN 5738 5774 BY SIMILARITY.
FT DOMAIN 5776 5812 BY SIMILARITY.
FT DOMAIN 5814 5850 BY SIMILARITY.
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FT DISULFID 575 589 BY SIMILARITY.
FT DISULFID 591 600 BY SIMILARITY.
FT DISULFID 602 618 BY SIMILARITY.
FT DISULFID 620 638 BY SIMILARITY.
FT DISULFID 640 655 BY SIMILARITY.
FT DISULFID 657 675 BY SIMILARITY.
FT DISULFID 677 693 BY SIMILARITY.
FT DISULFID 695 713 BY SIMILARITY.
FT DISULFID 715 730 BY SIMILARITY.
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FT DISULFID 770 788 BY SIMILARITY.
FT DISULFID 790 806 BY SIMILARITY.
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Note: remainder of annotations omitted.
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Query Match 17.3%; Score 154; DB 1; Length 2444;

Best Local Similarity 42.9%; Pred. No. 1.06e-12;

Matches 33; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

Db 2039 VNNVDAVLLKNGANKMONNRE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 2097

QY 3 MGNVHVAALLNTGADSNCEPTTFSPRHDAAAREGLDFLVVHGSGARLVDWAGRL 62

Db 2098 PRDIAQERHHDIVRL 2114

QY 63 PLDLAQERGHQDIVRYL 79

RESULT 13

ID NTC1_MOUSE STANDARD; PRT; 2531 AA.

AC 001705;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 13-JUL-1999 (Rel. 38, Last annotation update)

DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (NOTCH PROTEIN).

GN NOTCH1 OR NOTCH.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 1161 1204 EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1205 1245 EGF-LIKE 31.
FT DOMAIN 1247 1288 EGF-LIKE 32.
FT DOMAIN 1290 1326 EGF-LIKE 33.
FT DOMAIN 1336 1374 EGF-LIKE 34.
FT REPEAT 1388 1428 LIN/NOTCH 1.
FT REPEAT 1429 1467 LIN/NOTCH 2.
FT REPEAT 1468 1503 LIN/NOTCH 3.
FT REPEAT 1784 1816 CDC10/SWI6 1.
FT REPEAT 1817 1865 CDC10/SWI6 2.
FT REPEAT 1866 1898 CDC10/SWI6 3.
FT REPEAT 1899 1932 CDC10/SWI6 4.
FT REPEAT 1933 1965 CDC10/SWI6 5.
FT REPEAT 1966 1998 CDC10/SWI6 6.
FT DISULFID 43 55 BY SIMILARITY.
FT DISULFID 49 66 BY SIMILARITY.
FT DISULFID 68 77 BY SIMILARITY.
FT DISULFID 83 94 BY SIMILARITY.
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FT DISULFID 124 135 BY SIMILARITY.
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FT DISULFID 892 902 BY SIMILARITY.
FT DISULFID 897 911 BY SIMILARITY.
FT DISULFID 913 922 BY SIMILARITY.
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FT DISULFID 967 978 BY SIMILARITY.
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FT DISULFID 1345 1362 BY SIMILARITY.

Note: remainder of annotations omitted.

Query Match 16.5%; Score 147; DB 1; Length 2318;

Best Local Similarity 40.3%; Pred. No. 2.53e-11;

Matches 31; Conservative 14; Mismatches 31; Indels 1; Gaps 1;

Db 1950 VNNVEATLALLKNGANKMDSKE-ETPLFLAAREGSYENAKLLLDHLANREITDHLRL 2008

QY 3 MGNVHVAALLNTYGADSNCEPTTFSPRVHDAREGFLDTLVVLHGSGARLDYRDWGR 62

Db 2009 PRDVAQERHQDIVRL 2025

QY 63 PLDAQERHQDIVRYL 79

RESULT 15

ID NOTC_BRARE STANDARD; PRT; 2437 AA.

AC P46530;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN PRECURSOR.

GN NOTCH.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

OC Cyprinoidae; Cyprinidae; Rasbora; Danio.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=EMBRYO;

MPSRELH

(TM)

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MParch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:42:52 2000; MasPar time 16.56 Seconds
523.462 Million cell updates/sec

Tabular output not generated.

Title: >US-09-016-869A-6
Description: (1-125) from US09016869A.pep
Perfect Score: 892
Sequence: 1 MMGNVHVALLNYGADSN.....SFSSSTPRALRQGSQEQS 125

Scoring table: PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sprenb112
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 41.331; Variance 69.208; scale 0.597

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Query Match	Length	ID	Description	Pred. No.
1	892	100.0	168 11	P97510 CYCLIN DEPENDENT KINAS	1.74e-185
2	890	99.8	168 11	O89088 CYCLIN DEPENDENT KINAS	5.44e-185
3	806	90.4	113 11	Q921C2 CYCLIN-DEPENDENT KINAS	3.20e-164
4	492	55.2	102 6	O9X5S1 P15/CDKN2A/MTS1 (FRAGM	7.62e-88
5	488	54.7	86 6	O9X5S2 P15/MTS2/CDKN2B (FRAGM	6.86e-87
6	473	53.0	115 4	O16361 CELL CYCLE NEGATIVE RE	2.55e-83
7	461	51.7	86 11	O921C1 CYCLIN-DEPENDENT KINAS	1.80e-80
8	453	50.8	86 11	O54816 CYCLIN-DEPENDENT KINAS	1.42e-78
9	238	26.7	124 13	O9W618 P13CDKN2X.	2.15e-29
10	235	26.3	124 13	P70087 CDKN2X PROTEIN.	9.59e-29
11	214	24.0	58 6	O97886 CYCLIN-DEPENDENT KINAS	2.98e-24
12	163	18.3	835 4	O9Y2V6 HYPOTHETICAL 92.9 KD P	8.57e-14
13	160	17.9	251 11	O61905 NOTCH PROTEIN HOMOLOG	3.33e-13
14	156	17.5	1194 13	O9W737 NOTCH-1 (FRAGMENT).	2.01e-12
15	153	17.2	735 13	O93617 NOTCH HOMOLOGUE 2.	7.66e-12
16	152	17.0	2447 13	O13149 NOTCH 2 (FRAGMENT).	1.19e-11
17	148	16.6	389 11	O60941 NOTCH-2 (FRAGMENT).	6.99e-11
18	148	16.6	486 14	O96796 NOTCH2 (FRAGMENT).	6.99e-11
19	148	16.6	497 14	O96793 NOTCH2 (FRAGMENT).	6.99e-11
20	148	16.6	497 14	Q96794 NOTCH2 (FRAGMENT).	6.99e-11

21	148	16.6	547 14	O96795 NOTCH2 (FRAGMENT).	6.99e-11
22	148	16.6	638 4	Q04721 NEUROGENIC LOCUS NOTCH	6.99e-11
23	148	16.6	2470 11	O35516 CELL SURFACE PROTEIN.	6.99e-11
24	147	16.5	2321 4	Q9Y6L8 NOTCH3.	1.08e-10
25	146	16.4	683 13	O93616 KITAA0379 (FRAGMENT).	1.68e-10
26	144	16.1	882 4	O15084 NOTCH HOMOLOG (FRAGMEN	4.02e-10
27	143	16.0	248 5	O44115 NOTCH HOMOLOG (FRAGMEN	5.21e-10
28	138	15.5	1476 13	Q90285 NOTCH-3 HOMOLOG (FRAGM	5.37e-09
29	137	15.4	703 13	O93618 NOTCH HOMOLOGUE 3.	8.23e-09
30	136	15.2	1719 4	Q13768 ALT. ANKYRIN (VARIANT	1.26e-08
31	136	15.2	1848 11	O61302 ANKYRIN 1, ERYTHROID (1.26e-08
32	136	15.2	1856 4	O99407 ANKYRIN.	1.26e-08
33	134	15.0	654 11	O94261 SEX-DETERMINATION PROT	2.95e-08
34	133	14.9	1549 5	Q24241 ANKYRIN.	4.50e-08
35	131	14.7	1411 5	O02989 ALPHA-LATROINSECTOTOXI	1.04e-07
36	130	14.6	1088 4	Q13484 ANKYRIN G113.	1.59e-07
37	130	14.6	4377 4	O12955 ANKYRIN G.	1.59e-07
38	129	14.5	1786 5	O17344 UNC-44 (FRAGMENT).	2.41e-07
39	129	14.5	1809 5	O17487 E. ELEGANS ANKYRIN-REL	2.41e-07
40	129	14.5	1815 5	Q17488 C. ELEGANS ANKYRIN-REL	2.41e-07
41	129	14.5	1867 5	Q17486 C. ELEGANS ANKYRIN-REL	2.41e-07
42	129	14.5	2004 5	O61222 ZK1005.1 PROTEIN (FRAG	2.41e-07
43	129	14.5	2039 5	O17489 C. ELEGANS ANKYRIN-REL	2.41e-07
44	129	14.5	6994 5	O17343 UNC-44 ANKYRINS.	2.41e-07
45	127	14.2	1180 4	Q92625 MYELOBLAST KIAA0229 (F	5.53e-07

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	168 AA.
ID	P97510	PRELIMINARY;		
AC	P97510; P97937;			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR			
DE	PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16, INHIBITS CDK4			
DE	(P16INK4A) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).			
GN	CDKN2A OR ELAPHA OR P16INK4A OR CDKN2A.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-DBA/2N; TISSUE-SPLEEN;			
RA	MEDLINE; 98151529.			
RA	ZHANG S., RAMSAY E.S., MOCK B.A.;			
RT	"Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and			
RT	p19ARF, is a candidate for the plasmacytoma susceptibility locus,			
RT	Pctrl.,"			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).			
RL	[2]			
RP	SEQUENCE OF 1-42 FROM N.A.			
RC	STRAIN-VARIOUS STRAINS;			
RA	MEDLINE; 97179476.			
RA	HERZOG C.R., IOU M.;			
RT	"Sequence variation and chromosomal mapping of the murine Cdkn2a tumor			
RT	suppressor gene."			
RL	Mamm. Genome 8:65-66(1997).			
RN	[3]			
RP	SEQUENCE OF 1-155 FROM N.A.			
RC	STRAIN-C57BL/6J X DBA;			
RA	MALOMBRES M., DE CASTRO I., SANTOS J., MELENDEZ B., MANGUES R.,			
RA	SERRANO M., PELLICER A., FERNANDEZ-PIQUERAS J.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE OF 1-42 FROM N.A.			
RC	STRAIN-DBA/2 AND C57BL/6;			
RA	MEDLINE; 95380169.			
RA	QUELLE D.E., ASHMUN R.A., HANNON G.J., REHBERGER P.A., TRONO D.,			
RA	RICHTER K.H., WALKER C., BEACH D., SHERR C.J., SERRANO M.;			
RT	"Cloning and characterization of murine p16INK4a and p15INK4b genes."			
RL	Oncogene 11:635-645(1995).			

[5]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-DBA/2 AND C57BL/6;
RA GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN-ICR SWISS;
RX MEDLINE; 97128829.
RA SOLOFF E.V., HERZOG C.R., YOU M.;
RT "the 5'-flanking region of the El alpha form of the murine p16INK4a (MTS1) gene";
RL Gene 180:213-215(1996).
[7]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLF/EI AND MUS MUS MUSCULUS;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044336; AAC08963.1; -;
DR EMBL; AF04336; AAC08963.1; -;
DR EMBL; U49280; AAC00052.1; -;
DR EMBL; U66087; AAB39600.1; -;
DR EMBL; U66086; AAB39600.1; JOINED.
DR EMBL; AF004588; AAB61416.1; -;
DR EMBL; U47018; AAC52987.1; -;
DR EMBL; U79628; AAD00226.1; -;
DR EMBL; U79625; AAD00223.1; -;
DR EMBL; U79627; AAD00225.1; -;
DR HSSP; P42771; 1BI7.
DR MGD; MG1:104738; Cdkn2a.
DR PFAM; PF00023; ank; 3.
KW Kinase; Cyclin.
SQ SEQUENCE 168 AA; 17941 MW; 89AD5E62 CRC32;

Query Match 100.0%; Score 892; DB 11; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.74e-185;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG 103
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG 60
|||||
Db 104 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTGCHFSSTPRALELRGQ 163
QY 61 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTGCHFSSTPRALELRGQ 120
|||||
Db 164 SQEQS 168
QY 121 SQEQS 125
|||||

RESULT 2 PRELIMINARY; PRT; 168 AA.
ID O89088
AC O89088;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
GN CDKN2A OR E1ALPHA OR P16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CANPT; TISSUE-SPLEEN;
RX MEDLINE; 98151529.
RA ZHANG S., RAMSAY E.S., MOCK B.A.;
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus, Petrl.";

Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
[2]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-WA/W4J;
RX MEDLINE; 97179476.
RA HERZOG C.R., YOU M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor suppressor gene";
RL Mamm. Genome 8:65-66(1997).
[3]
RP SEQUENCE OF 1-42 FROM N.A.
RC STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF044335; AAC08962.1; -;
DR EMBL; U49279; AAC00051.1; -;
DR EMBL; U79626; AAD00224.1; -;
DR HSSP; P42771; 1BI7.
DR PFAM; PF00023; ank; 3.
KW Kinase; Cyclin.
SQ SEQUENCE 168 AA; 17915 MW; F0087F4C CRC32;

Query Match 99.8%; Score 890; DB 11; Length 168;
Best Local Similarity 99.2%; Pred. No. 5.44e-185;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 44 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG 103
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG 60
|||||
Db 104 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTGCHFSSTPRALELRGQ 163
QY 61 RLPLDLAQRGHQDIVRYLSAGCSLCSAGWSLCTAGNVAQTGCHFSSTPRALELRGQ 120
|||||
Db 164 SQEQS 168
QY 121 SQEQS 125
|||||

RESULT 3 PRELIMINARY; PRT; 113 AA.
ID Q921C2
AC Q921C2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P16.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRET/EI;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79634; AAD00236.1; -;
DR HSSP; P42771; 1BI7.
DR EMBL; U79634; AAD00236.1; -;
KW Kinase; Cyclin.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12073 MW; 1D82E6DF CRC32;

Query Match 90.4%; Score 806; DB 11; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.20e-164;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVDRDAG 61

|||||
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60
DB 62 RLPLDLAQRGHQDIVYRLSAGCSAGWSLCTAGNVAQTDGHSFSSSTP 113
|||||
QY 61 RLPLDLAQRGHQDIVYRLSAGCSAGWSLCTAGNVAQTDGHSFSSSTP 112

RESULT 4
ID Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
RT and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 102 AA; 10824 MW; 8C3094E9 CRC32;

Query Match 55.2%; Score 492; DB 6; Length 102;
Best Local Similarity 79.0%; Pred. No. 7.62e-88;
Matches 64; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
DB 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61
|||||
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60
DB 62 RLPLDLAQRGHQDIVYRLSAG 82
|||||
QY 61 RLPLDLAQRGHQDIVYRLS 81

RESULT 5
ID Q9XS52 PRELIMINARY; PRT; 86 AA.
AC Q9XS52;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RA OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
RA NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
RT and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 86 AA; 9340 MW; 8C5D01A0 CRC32;

Query Match 54.7%; Score 488; DB 6; Length 86;
Best Local Similarity 75.9%; Pred. No. 6.86e-87;
Matches 63; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
DB 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61
|||||
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60

DB 62 RLPLDLAQRGHQDIVYRLSAG 84
|||||
QY 61 RLPLDLAQRGHQDIVYRLSAG 83

RESULT 6
ID Q16361 PRELIMINARY; PRT; 115 AA.
AC Q16361;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE CELL CYCLE NEGATIVE REGULATOR BETA FORM (FRAGMENT).
GN P16/MTS1/CDKN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9530726.
RA STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,
RA PARRY D., PETERS G., KAMB A.;
RT "Complex structure and regulation of the p16 (MTS1) locus.";
RL Cancer Res. 55:2988-2994(1995).
DR EMBL; S78535; AAC60650.1; -.
DR HSP; P42771; IBI7.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 115 AA; 12334 MW; F5BEF54B CRC32;

Query Match 53.0%; Score 473; DB 4; Length 115;
Best Local Similarity 73.5%; Pred. No. 2.55e-83;
Matches 61; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
DB 11 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 70
|||||
QY 1 MMGNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTLVVLHSGARLDVWDANG 60
DB 71 RLPLDLAQRGHQDIVYRLSAG 93
|||||
QY 61 RLPLDLAQRGHQDIVYRLSAG 83

RESULT 7
ID Q921C1 PRELIMINARY; PRT; 86 AA.
AC Q921C1;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN P15.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RA SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
RA PELLICER A., FERNANDEZ-PIQUERAS J.;
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT in mouse inbred strains.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U79637; AAD00237.1; -.
DR HSP; P42771; IBI7.
KW Kinase; Cyclin.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9269 MW; D5811BE2 CRC32;

Query Match 51.7%; Score 461; DB 11; Length 86;
Best Local Similarity 73.2%; Pred. No. 1.80e-80;
Matches 60; Conservative 14; Mismatches 8; Indels 0; Gaps 0;
DB 2 MMGSAVVAELLLHGAENPCADPATLTPRVHDAAREGFLDTLVVLHSGARLDVWDANG 61

Search completed: Thu Jul 20 08:43:12 2000

Job time : 20 secs.

OM of: US-09-016-869A-6 to: GenEmbl.* out_format : pfs
Date: Jul 21, 2000 8:05 AM
About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
-MODEL=frame-pzn.model -DEV=xlp
-Q/cgn2_1/USPTO_spool/US09016869/runat_20072000_083606_16071/app_query.fasta_1.598
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=45 -DLOCALIGN=200 -THR_SCORE=pcr -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=100000 -USER=US09016869 @cgn1_1_3917 -NCPU=6 -ICPU=3
-LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-016-869A-6
Query length: 125
Database: GenEmbl.*
Database sequences: 972840
Database length: 892348106
Search time (sec): 1513.910000

score_list:

Sequence	Strd Orig	Score	Escore	Len	Documentation
gb_pat:AR062814	+ 658.00	1135.40	3.8e-55	507	AR062814 Sequence 44 from patent
gb_pat:US9920	+ 658.00	1132.64	5.4e-55	713	I89920 Sequence 1 from patent
gb_ro:MUSARF	+ 658.00	1132.64	5.4e-55	713	I76092 Mus musculus p19 ARF p19
gb_ro:S080650	+ 658.00	1132.64	5.4e-55	713	I80650 p16INK4a-CDK4 and CDK6
gb_ro:MUSP16INK	+ 658.00	1131.26	6.5e-55	846	I76150 Mus musculus CDK4 and CDK6
gb_ro:AF044336	+ 658.00	1131.23	6.5e-55	849	AF044336 Mus musculus strain DE
gb_ro:AF044335	+ 657.00	1129.50	8.1e-55	849	AF044335 Mus musculus strain BA
gb_ro:NMINK4A02	+ 602.00	1039.01	8.9e-50	482	I66087 Mus musculus cyclin-depe
gb_ro:NMU79634	+ 597.00	1033.21	1.9e-48	339	I79634 Mus spretus cyclin-depe
gb_ro:NMU79633	+ 583.00	1009.01	4.2e-48	339	I79633 Mus musculus cyclin-depe
gb_ro:NMU79630	+ 579.00	1002.10	1.0e-47	339	I79630 Mus musculus cyclin-depe
gb_ro:NMU79631	+ 578.00	1000.37	1.3e-47	339	I79631 Mus musculus cyclin-depe
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gb_ro:NMU79635	+ 572.50	990.94	4.2e-47	336	I79635 Mus musculus cyclin-depe
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gb_pat:AR001335	+ 445.00	769.25	9.5e-35	395	AR001335 Sequence 25 from patent
gb_pat:AR037515	+ 445.00	769.25	9.5e-35	395	AR037515 Sequence 25 from patent
gb_pat:AR062795	+ 445.00	769.25	9.5e-35	395	AR062795 Sequence 25 from patent
gb_pat:I41169	+ 445.00	769.25	9.5e-35	395	I41169 Sequence 25 from patent
em_com:AB010808	+ 345.00	591.31	7.7e-25	742	AB010808 Felis catus gene for p
gb_pat:SC242787	+ 342.00	590.82	8.2e-25	415	AJ242787 Sus scrofa cdkn2a gene
em_com:AB010807	+ 341.00	593.30	2.2e-24	850	AB010807 Felis catus gene for p
gb_pat:AR001316	+ 338.50	576.28	5.3e-24	1187	AR001316 Sequence 4 from patent
gb_pat:AR037496	+ 338.50	576.28	5.3e-24	1187	AR037496 Sequence 4 from patent
gb_pat:AR062776	+ 338.50	576.28	5.3e-24	1187	AR062776 Sequence 4 from patent
gb_pat:I41150	+ 335.50	576.82	5.3e-24	1187	I41150 Sequence 4 from patent
gb_pr3:HSPCDK2	+ 335.50	576.81	4.9e-24	585	I14181 Human p16-INK4 (p16) gen
gb_pr4:AF011544	+ 335.50	543.83	3.4e-22	34669	IAC000048 Homo sapiens Chromos
gb_pr4:AF011544	+ 332.00	568.30	1.5e-23	793	AF011544 Homo sapiens cyclin-de
gb_pat:AR001346	+ 332.00	566.87	1.8e-23	947	AR001346 Sequence 36 from patent
gb_pat:AR037526	+ 332.00	566.87	1.8e-23	947	AR037526 Sequence 36 from patent
gb_pat:AR062806	+ 332.00	566.87	1.8e-23	947	AR062806 Sequence 36 from patent
gb_pat:I41180	+ 332.00	566.87	1.8e-23	947	I41180 Sequence 36 from patent
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gb_pr2:HSU26727	+ 332.00	566.29	1.9e-23	1017	I26727 Human p16INK4/MTS1 mRNA
gb_pat:AR001345	+ 332.00	565.44	2.1e-23	1131	AR001345 Sequence 13 from patent
gb_pat:AR037505	+ 332.00	565.44	2.1e-23	1131	AR037505 Sequence 13 from patent
gb_pat:AR062785	+ 332.00	565.44	2.1e-23	1131	AR062785 Sequence 13 from patent
gb_pat:I41159	+ 332.00	565.44	2.1e-23	1131	I41159 Sequence 13 from patent
gb_pat:I67718	+ 332.00	563.60	2.7e-23	1420	I67718 Sequence 1 from patent
gb_pat:AR001314	+ 330.00	569.06	1.3e-23	471	AR001314 Sequence 1 from patent

gb_pat:AR037494 + 330.00 569.06 1.3e-23 471 AR037494 Sequence 1 from pat
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seq_name: gb_pat:AR062814

seq_documentation_block: 507 bp DNA PAT 29-SEP-1999

LOCUS AR062814

DEFINITION Sequence 44 from patent US 5843756.

ACCESSION AR062814

VERSION AR062814.1 GI:5990505

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 507)

AUTHORS Stone, S., Jiang, P. and Kamb, A.

TITLE Mouse MTS1 gene

JOURNAL Patent: US 5843756-A 44 01-DEC-1998;

FEATURES Location/Qualifiers

Source

1..507

BASE COUNT 86 a 157 c 165 g 99 t

ORIGIN

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Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-016-869A-6 x AR062814

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17 aASpSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34

180 AGATTCGAACTCCGAGGACCCACCTACCTTCTCCGCGCCGGTGCACGACG 229

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlyserGly 50

230 CAGCGCGGAAGGCTTCCTGCACACGCTGGTGTCTGCACGGGTTCAGGG 279

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67

280 GCTCGGTGGATGTCCGGATGCTGGGGTCCCTCCGCTCGACTTGGC 329

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84

330 CCAGAGCGGGGACATCAAGACATCGTGGGATATTTGGTTCCTCCGCTGGGT 379

84 ySSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100

380 GCTCTTTGTCTCCGCTGGGTGGTCTTTGTCTACCGCTGGGACGCTGCC 429

101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117

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seq_name: gb_pat:I89920

seq_documentation_block: 713 bp DNA PAT 10-AUG-1998

LOCUS I89920

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DEFINITION Sequence 1 from patent US 5723313.
ACCESSION 189920
VERSION 189920.1 GI:3409860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 713)
  Sherr,C.J. and Quelle,D.E.
  ARF-p19, a novel regulator of the mammalian cell cycle
  Patent: US 5723313-A 1 03-MAR-1998;
  JOURNAL Location/Qualifiers
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      /note="arginine-rich protein"
      /codon_start=1
      /function="G1 and G2 phase cell cycle arrest in fibroblast"
      /evidence=experimental
      /product="p19 ARF protein"
      /protein_id="AAC42080.1"
      /db_xref="GI:1162947"
      /translation="MGRRLVTVRIQAGRELFQVFLKFRSRRPRTASCALAFVN
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BASE COUNT 133 a 194 c 224 g 162 t
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    17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
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      286 AGATTCGAACGCGAGAGCCCACTACCTTCTCCGCCCGGTGCAGCAGC 335
    34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
      |||
      336 CACGCGGGGAAGCTTCCTGGACACGCTGGTGTGTCACGCGGTGACGGG 385
    51 AlaArgLeuAspValArgAspAlaTrrpGlyArgLeuProLeuAspLeuAl 67
      |||
      386 GCTCGGCTGGATGTCGCGATCGTCGATATTTGCTGCCCTCGACTTGGC 435
    67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
      |||
      436 CCAAGAGCGGGGACATCAAGACATCGTCGATATTTGCTGCCCTCGACTTGGC 485
    84 ySerLeuCysSerAlaGlyTrrpSerLeuCysThrAlaGlyAsnValAla 100
      |||
      486 GCTCTTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGACCTGGAAC 535
    101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
      |||
      536 CAGACCGAGCGGCATAGCTTACGTCACGACGCCCGGCGGCTGGAACCT 585
    117 uArgGlyGlnSerGlnGlnSer 125
      |||
      586 TCGCGGCCAATCCACAGACGAGCAGC 610
  seq_name: gb_ro:MUSARF

seq_documentation_block:
  LOCUS MUSARF 713 bp mRNA ROD 20-JAN-1996
  DEFINITION Mus musculus p19 ARF protein mRNA, complete cds.
  ACCESSION L76092
  VERSION L76092.1 GI:1162946
  KEYWORDS p19 protein.
  SOURCE Mus musculus (clone: MARF) cDNA to mRNA.
  ORGANISM Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE
    1 (bases 1 to 713)
    Quelle,D.E., Zindy,F., Ashmun,R.A. and Sherr,C.J.
    Alternative reading frames of the INK4a tumor suppressor gene
    encode two unrelated proteins capable of inducing cell cycle arrest
    Cell 83 (6), 993-1000 (1995),
    JOURNAL Location/Qualifiers
    MEDLINE 96107337
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BASE COUNT 133 a 195 c 223 g 162 t
ORIGIN

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    34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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    67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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      436 CCAAGAGCGGGGACATCAAGACATCGTCGATATTTGCTGCCCTCGACTTGGC 485
    84 ySerLeuCysSerAlaGlyTrrpSerLeuCysThrAlaGlyAsnValAla 100
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      486 GCTCTTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGACCTGGAAC 535
    101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
      |||
      536 CAGACCGAGCGGCATAGCTTACGTCACGACGCCCGGCGGCTGGAACCT 585
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LOCUS      S80650      713 bp      mRNA      ROD      02-APR-1996
DEFINITION p16INK4a-CDK4 and CDK6 cyclin D-dependent kinases inhibitor
            (alternatively spliced, exon 1 beta and exon 2) [mice, MEL
            erythroleukemia cells, mRNA Partial, 713 nt].
ACCESSION  S80650
VERSION    C611 83 (6), 993-1000 (1995)
KEYWORDS   S80650.1 GI:1245977
SOURCE     Mus sp. MEL erythroleukemia cells.
ORGANISM   Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 713)
AUTHORS   Quelle,D.E., Zindy,F., Ashmun,R.A. and Sherr,C.J.
TITLE     Alternative reading frames of the INK4a tumor suppressor gene
            encode two unrelated proteins capable of inducing cell cycle arrest
JOURNAL   Cell 83 (6), 993-1000 (1995)
MEDLINE   96107337
REMARK    GenBank staff at the National Library of Medicine created this
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            This sequence comes from Fig. 2.
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               /db_xref="GI:1245978"
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BASE COUNT 133 a 195 c 223 g 162 t
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51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
436 CCAAGACGCGGGACATCAAGACATCGTGGCATATTTTCGCTTCGCTGGGT 485
84 ySerLeuCysserAlaGlyTyrPsrLeuLeuCysThrAlaGlyAsnValAla 100

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486 GCTCTTTGTGTTCCCTGGTGGTCTTTGTGTACCGCTGGGAACGTGCGC 535
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
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586 TCGCGGCCAATCCCAAGAGCAGAGC 610
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seq_documentation_block:
LOCUS      MUSP16INK      846 bp      mRNA      ROD      20-JAN-1996
DEFINITION Mus musculus CDK4 and CDK6 inhibitor protein (p16INK4a) mRNA,
            complete cds.
ACCESSION  L76150
VERSION    L76150.1 GI:1162948
KEYWORDS   CDK4 inhibitor; CDK6 inhibitor.
SOURCE     Mus musculus cDNA to mRNA.
ORGANISM   Mus musculus
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            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 846)
AUTHORS   Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rehberger,P.A., Trono,D.,
            Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M.
            Cloning and characterization of murine p16INK4a and p15INK4b genes
JOURNAL   Oncogene 11 (4), 635-645 (1995)
MEDLINE   95380169
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17 aspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
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67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
408 CCAGAGCGGGGACATCAAGACATCGTCGGATATTGCGTTCGGTGGGT 457
84 ySerLeuCysSerAlaGlyTTPSerLeuCysThrAlaGlyAsnValAla 100
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101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
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558 TCGCGGCCAATCCCAAGACGAGAGC 582
seq_name: gb_ro:AF044336
seq_documentation_block:
LOCUS AF044336 849 bp mRNA ROD 01-APR-1998
DEFINITION Mus musculus strain DBA/2N cyclin dependent kinase inhibitor
p16INK4a (Cdkn2a) mRNA, complete cds.
ACCESSION AF044336
VERSION AF044336.1 GI:3002948
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)
and p19(ARF), is a candidate for the plasmacytoma susceptibility
locus, pctl1
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)
MEDLINE 98151529
REFERENCE
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1998) NCI/IG, NIH, 37 Convent Dr., Bethesda, MD
20892, USA
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51 AlaArgLeuAspValArgAspAlaTTPGlyAcqLeuProLeuAspLeuAl 67
361 GCTCGGCTGGATGTGCGGATGCTGCGGTGCGCTGCCGCTGACTTGGC 410
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411 CCAGAGCGGGGACATCAAGACATCGTCGGATATTGCGTTCGGTGGGT 460
84 ySerLeuCysSerAlaGlyTTPSerLeuCysThrAlaGlyAsnValAla 100
461 GCTCTTTGTTCCGCTGGGTGCTCTTTGTACCGCTGGGAACGTCGCC 510
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
511 CAGACCGCGGGCATAGCTTCAGCTCAGACACGCCCGAGGCGCTTGA 560
117 uArgGlyGlnSerGlnGlnSer 125
561 TCGCGGCCAATCCCAAGACGAGAGC 585
seq_name: gb_ro:AF044335
seq_documentation_block:
LOCUS AF044335 849 bp mRNA ROD 01-APR-1998
DEFINITION Mus musculus strain BALB/cAnPt cyclin dependent kinase inhibitor
p16INK4a (Cdkn2a) mRNA, complete cds.
ACCESSION AF044335
VERSION AF044335.1 GI:3002946
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)
and p19(ARF), is a candidate for the plasmacytoma susceptibility
locus, pctl1
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)
MEDLINE 98151529
REFERENCE
AUTHORS Zhang,S., Ramsay,E.S. and Mock,B.A.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-1998) NCI/IG, NIH, 37 Convent Dr., Bethesda, MD
20892, USA
FEATURES
source
1. .849
/organism="Mus musculus"
/strain="BALB/cAnPt"
/db_xref="taxon:10090"

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82. .588
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/translation="MESADRLARAAGRVDPVRLLEAGVSPNAPSFGRTPIQVM
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RQSQEQS"
BASE COUNT 188 a 217 c 272 g 172 t
ORIGIN

alignment_scores:
  Quality: 657.00      Length: 125
  Ratio: 5.256         Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.200

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1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuAsnTyrGlyAl 17
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17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
261 AGATTCGAACCTGCGAGACCCCACTACTCTCCCGCCGGTGCACGACG 310

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
311 CAGCGCGGAAGGCTTCCTGCACACGCTGGTGTGCTGCACGGGTGACGG 360

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
361 GCTCGGCTGGATGTCGCGATGCTGGGGTGCCTGCCGCTCGACTGGC 410

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
411 CCAAGACGGGGGACATCAAGACATCGTGGGATATTGCGTTCGCTGGGT 460

84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100
461 GCTCTTTGTGTTCGCTGGGTGGTCTTTGTGTACCGCTGGGAACGTCGCC 510

101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
511 CAGACCGACGGGCATAGCTTCAGCTCAGACACGCCCGCCGCTGGAACT 560

117 uArgGlyGlnSerGlnGluGlnSer 125
561 TCGGGGCCAATCCCAAGACGACAGC 585

seq_name: gb_ro:MMINK4A02
seq documentation_block: 482 bp DNA ROD 02-JAN-1997
LOCUS MMINK4A02
DEFINITION Mus musculus cyclin-dependent kinase inhibitor (p16INK4a) gene,
exon 2 and partial cds.
ACCESSION U66087
VERSION U66087.1 GI:1762922
KEYWORDS
SEGMENT 2 of 2
SOURCE house mouse.
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 482)
AUTHORS Malumbres,M., Perez de Castro,I., Santos,J., Melendez,B.,
Manques,R., Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Inactivation of the cyclin-dependent kinase inhibitor p16INK4b by
deletion and de novo methylation with independence of p16INK4a
alterations in murine primary T-cell lymphomas
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 482)
AUTHORS Malumbres,M. and Pellicer,A.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1996) Pathology (MSB 594), New York University
Medical Center, 550 First Avenue, New York, NY 10016, USA
FEATURES
Location/Qualifiers
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/db_xref="taxon:10090"
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/codon_start=1
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BASE COUNT 81 a 138 c 143 g 120 t
ORIGIN

alignment_scores:
Quality: 602.00 Length: 113
Ratio: 5.327 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-016-869A-6 x MMINK4A02 ..
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107 ATGATGATGGCAACGTTTCAGTAGCAGCTCTTCTGCTCAACTACGGTGC 156
17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
157 AGATTCGAACCTGCGAGACCCCACTACTCTCCCGCCGGTGCACGACG 206
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
207 CAGCGCGGAAGGCTTCCTGCACACGCTGGTGTGCTGCACGGGTGACGG 256
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
257 GCTCGGCTGGATGTCGCGATGCTGGGGTGCCTGCCGCTCGACTTGGC 306
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
307 CCAAGACGGGGGACATCAAGACATCGTGGGATATTGCGTTCGCTGGGT 356
84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100
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357 GCTCTTTGTGTCCTGGTGGTCTTCTGTGTACCGTGGGAACGTCGCC 406
101 GlnThrAspGlyHisSerPheSerSerThrProArg 113
|||||
104 CAGCGCGGAAGGCTTCTGTGCACACGCTGTGTGTGTCGACGGTCAAGG 153
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
|||||
154 GCTCGGCTGGATGCGCGATGCTGGGGTCGCGTCCGCTCGACTTGGC 203
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
204 CCAGACGGGGACATCAACACATCGTCCGATATTTCGCTCCGCTGGGT 253
84 ySerLeuCySerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
|||||
254 GCTCTTTGTGTCCTGGTGGTCTTGTGTACCGTGGGAACGTCGCC 303
101 GlnThrAspGlyHisSerPheSerSerThrPro 112
|||||
304 CAGACCGACGGGATAGCTTCAGTCAAGCACGCC 339
seq_name: gb_ro:MSU79634
seq_documentation_block: 339 bp DNA ROD 05-JAN-1999
LOCUS MSU79634 Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
DEFINITION gene, exon 2 and partial cds.
ACCESSION U79634
VERSION U79634.1 GI:4098165
KEYWORDS western wild mouse.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A., and Fernandez-Piqueras, J.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
FEATURES
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/strain="SPRET/EI"
/db_xref="taxon:10096"
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/number=2
<1..>339
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/db_xref="GI:4098166"
/translation="VMMGMNVHVAALLNYGADSNCEPTTFSRPVHDAAREGFLDTL
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TDGHSFSSSTP"
BASE COUNT 54 a 101 c 111 g 73 t
ORIGIN
alignment_scores:
Quality: 597.00 Length: 112
Ratio: 5.330 Caps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-016-869a-6 x MSU79634 ..
Align seg 1/1 to: MSU79634 from: 1 to: 339
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4 ATGATGATGGGCAACGCTACATAGCAGCTCTCTGCTCAACTACGGTGC 53
17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
|||||
54 AGATTTCGAACTCGAGGAGCCCACTACCTTCTCCCGCCCGGTGCACGACG 103
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[illegible]

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100
 380 GCTCTTTGTGTTCCGCTGGTGGTCTTTGTGTACCGTGGGAACGTCGCC 429
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLeu 117
 430 CAGACCGACGGGCATAGCTTCAGCTCAAGCACGCCCGAGGCCCTGGAAC 479
 117 uArgGlyGlnSerGlnGluGlnSer 125
 480 TCGCGGCCAATCCCAAGACGAGCAGC 504

seq_name: N_Geneseq_36:T62485

seq_documentation_block:

ID T62485 standard; CDNA; 713 BP.
 AC T62485;
 DT 16-AUG-1997 (first entry)
 DE Murine ARF-p19 CDNA.
 KW ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis;
 KW gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;
 KW inhibitor; ss.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT cds 43..552
 FT /*tag= a
 FT /product= ARF-p19
 FT cds 236..613
 FT /*tag= b
 FT /product= INK4a-p16 C-terminal fragment
 FT exon 1..232
 FT /*tag= c
 FT /note= "Exon 1-beta"
 FT exon 233..702
 FT /*tag= d
 FT /note= "Exon 2"
 FT primer_bind complement(56..75)
 FT /*tag= e
 FT /note= "5' primer for RT-PCR"
 FT primer_bind 602..624
 FT /*tag= f
 FT /note= "3' primer for RT-PCR"

W09712060-A1.

PN 03-APR-1997.
 PD 25-SEP-1996; U15312.
 PF 27-SEP-1995; US-534975.
 PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PI Quelle DE, Sherr CJ;
 DR WPI; 97-212919/19.
 DR P-PSDB; W16321-22.
 PT Nucleic acid encoding ARF-p19 which induces cell cycle arrest when
 PT overexpressed - used for diagnosis and treatment of cancer, and for
 PT drug screening
 PS Claim 2; Fig 1; 49pp; English.
 CC A murine CDNA molecule (T62485) homologous to human INK4A beta
 CC transcripts (see also T62486) was isolated from a mouse
 CC erythroleukaemia cell DNA library. Sequences of exon 1-beta are
 CC spliced to exon 2 to create an open reading frame that encodes a
 CC novel protein, ARF-p19 (W16321), which induces cell cycle arrest
 CC when overexpressed. Unrelated sequences from exon 1-alpha (not
 CC shown) are spliced to the same exon 2 acceptor site to open another
 CC reading frame that encodes INK4a-p16 (C-terminal fragment given in
 CC W16322), an inhibitor of the cyclin D-dependent kinases CDK4 and
 CC CDK6. Economical reutilisation of protein coding sequences in this
 CC manner is without precedent in mammalian genomes and the unitary
 CC inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement
 CC for both proteins in cell cycle control. ARF-p19 nucleic acids can
 CC be used as probes or primers, or in gene therapy protocols to
 CC induce cell arrest in eukaryotes or (antisense) to inhibit ARF-p19
 CC activity, and to create transgenic animals useful as models for
 CC cancer. Human ARF-p19 CDNA (T62486) has also been isolated.
 CC Sequence 713 BP; 133 A; 195 C; 223 G; 162 T;

alignment_scores:
 Quality: 658.00 Length: 125
 Ratio: 5.264 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-016-869a-6 x T62485 ..
 Align seg 1/1 to: T62485 from: 1 to: 713
 1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
 236 ATGATGATGGCAACGTTACGTAGCAGCTCTTCTGCTCAACTACGCTGC 285
 17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
 286 AGATTGCACTGCGAGGACCCCTACCTTCTCCCGCCGGTGCACGACG 335
 34 laAlaargGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
 336 CAGCGCGGGAAGCTTCTTGGACACGCTGGTGGTGTGCACGGGTGAGG 385
 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
 386 GCTCGGCTGGATGTCGCGCATGCTGGGGTGGCTGCGCTCGACTTGGC 435
 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
 436 CCAGAGCGGGGACATCAAGACATCGTCGATATTTGCGTTCGCTGGGT 485
 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
 486 GCCTCTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGACGTCGCC 535
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLeu 117
 536 CAGACCGACGGGCATAGCTTCAGCTCAAGCACGCCCGAGGCCCTGGAAC 585
 117 uArgGlyGlnSerGlnGluGlnSer 125
 586 TCGCGGCCAATCCCAAGACGAGCAGC 610

seq_name: N_Geneseq_36:T02965

seq_documentation_block:

ID T02965 standard; CDNA; 853 BP.
 AC T02965;
 DT 01-MAR-1996 (first entry)
 DE Cell-cycle regulatory protein p13.5 cDNA.
 KW Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
 KW CCR; gene therapy; transgenic animal; cancer; cell proliferation;
 KW ss; ds.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT cds 213..590
 FT /*tag= a
 PN W09528483-A1.
 PD 26-OCT-1995.
 PF 14-APR-1995; U04536.
 PR 14-APR-1994; US-227371.
 PR 25-MAY-1994; US-248812.
 PR 14-SEP-1994; US-306511.
 PR 29-NOV-1994; US-346147.
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Beach DH, Demetrick DU, Hannon GJ, Serrano M;
 DR WPI; 95-373798/48.
 DR P-PSDB; R85120.
 PT New cell cycle regulating proteins bind to cyclin dependent kinase -
 PT and related nucleic acids, antibodies etc., used in diagnosis and
 PT therapy of abnormal cell proliferation, degeneration etc.
 PT Example 4; Page 80; 109pp; English.

CC cDNA (T02965) coding for the mouse cell-cycle regulatory (CCR)
 CC protein p13.5 (R85120) was isolated from an embryonal stem cell
 CC library using a probe based on human CCR p16 cDNA (T02962).
 CC The isolated cDNA can be used: to detect mutations in CCR
 CC genes that lead to cell proliferation; to breed transgenic
 CC animals to study cellular disorders involving CCR allele
 CC mutation/misexpression; and to correct CCR-deficient cells
 CC (gene therapy).
 SQ Sequence 853 BP: 192 A: 207 C: 274 G: 180 T:

alignment_scores:
 Quality: 558.00 Length: 125
 Ratio: 5.264 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-016-869A-6 x T02965 ..

Align seg 1/1 to: T02965 from: 1 to: 853

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17 aaSpSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
263 AGATTCGAACCTGGGAGGACCCACTACTCTTCCCGCCGGTGCACGACG 312

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
313 CAGCGCGGGAAGGCTTCTTGACACGCTGGTGTGCTGCACGGGTACGGG 362

51 AlaArgLeuAspValArgAspAlaTirPglyArgLeuProLeuAspLeuAl 67
|||||
363 GCTCGGCTGGATGTCGCGATGCTCGGGGTGCGCTGCGGCTCGACTGGC 412

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
413 CCAAGAGCGGGGACATCAAGACATCGTGCATATTTGCGTTCCTCGGT 462

84 ySerLeuCySerAlaGlyTirPserLeuCyThrAlaGlyAsnValAla 100
|||||
463 GCTCTTGTGTTCGCTGGGTGGTGTGTGTGTACCGCTGGGAACGTCGCC 512

101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
|||||
513 CAGACCCAGCGGCATAGCTTCAGCTCAAGCAGCCCGGCGCCCTGGAACT 562

117 uArgGlyGlnSerGlnGlnSer 125
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563 TCGCGGCAATCCCAAGACGACGACG 587

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seq_name: N_Geneseq_36.V11259

seq_documentation_block:

ID V11259 standard; cDNA; 395 BP.
 AC V11259;
 DT 15-JUL-1998 (first entry)
 DE Mouse p16 cDNA fragment.
 KW MTS1; MTS2; MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
 KW germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
 OS Mus sp.
 PN US5739027-A.
 PD 14-APR-1998.
 PF 07-JUN-1995; 487033.
 PR 07-JUN-1995; US-487033.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.

PA (MYRI-) MYRIAD GENETICS INC.
 PI Kamb A;
 DR WPI; 98-250421/22.
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
 PT useful for the diagnosis of cancers related to MTS1E1-beta
 PT mutation(s) and their treatment
 PS Disclosure; Figure 14; 72pp; English.
 CC This is a mouse p16 cDNA sequence used in the characterisation of the
 CC human multiple tumour suppression proteins, MTS1, MTS2 and MTS1E1-beta.
 CC The MTS gene locus is also referred to as the familial melanoma (MLM)
 CC gene locus, located on human chromosome 9p21. Germ line mutations in
 CC MTS genes can be used in the diagnosis of predisposition to cancers.
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
 CC ovary, uterus, testis, kidney, stomach and rectum.
 SQ Sequence 395 BP: 73 A: 109 C: 128 G: 85 T:

alignment_scores:

Quality: 445.00 Length: 85
 Ratio: 5.235 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.824

alignment_block:

US-09-016-869A-6 x V11259 ..

Align seg 1/1 to: V11259 from: 1 to: 395

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1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
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140 ATGATGATGGCAACGTTACGTAGCAGCTTCTGCTCAACTACGGTGC 189

17 aaSpSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTCGAACCTGGGAGGACCCACTACTCTTCCCGCCGGTGCACGACG 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGGAAGGCTTCTTGACACGCTGGTGTGCTGCACGGGTACGGG 289

51 AlaArgLeuAspValArgAspAlaTirPglyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGGCTGGATGTCGCGATGCTCGGGGTGCGCTCCCGCTCGACTCGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
340 CCAAGAGCGGGGACATCAAGACATCGTGCATATTTGCGTTCCTCGGT 389

84 ySer 85
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390 GCTCT 394

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seq_name: N_Geneseq_36.V53840

seq_documentation_block:

ID V53840 standard; DNA; 395 BP.
 AC V53840;
 DT 04-DEC-1998 (first entry)
 DE Nucleotide sequence of nucleic acid 6.
 KW Multiple tumour suppressor; MTS1E1S; human; cancer; hybridisation;
 KW somatic mutation; gene therapy; ds.
 OS Homo sapiens.
 PN US5801236-A.
 PD 01-SEP-1998.
 PF 07-JUN-1995; 480810.
 PR 07-JUN-1995; US-480810.
 PR 18-MAR-1994; US-214582.
 PR 18-MAR-1994; US-215086.
 PR 18-MAR-1994; US-215087.
 PR 14-APR-1994; US-227369.
 PR 01-JUN-1994; US-251938.
 PR 17-MAR-1995; WO-U03316.
 PA (MYRI-) MYRIAD GENETICS INC.

PI Kamb A;
DR WPI; 98-494842/42.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Disclosure; Column 83-84; 73pp; English.
CC This is the nucleotide sequence of a nucleic acid used in the
CC method of the invention involving the use of the multiple tumour
CC suppressor (MTS) gene to diagnose and treat human cancers. The MTS
CC gene is useful in the diagnosis and prognosis of human cancer, e.g.
CC by standard nucleic hybridisation techniques, of patient samples.
CC The mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

alignment_scores:
Quality: 445.00 Length: 85
Ratio: 5.235 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.824

alignment_block:
US-09-016-869A-6 x V53840 ..

Align seg 1/1 to: V53840 from: 1 to: 395

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1 MetMetMetClyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
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17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTGCAACTCGAGGACCCCACTACCTTCTCCGCCCGGTGCAGGAC 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGAAGGCTTCTCGGACACGCTGGTGTGCTGCACGGGTACGG 289

51 AlaArgLeuAspValArgAspAlaTrrpGlyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGCTGGATGTCGCGATGCTCGGGTGGCTCCCTCCGCTCGACTTGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
340 CCAAGAGCGGGGACATCAAGACATCGTGCATATTGCGTTCCGCTGGGT 389

84 ySser 85
|||||
390 GCTCT 394
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seq_name: N_Geneseq_36:V70604

seq_documentation_block:

ID V70604; standard; cDNA; 395 BP.
AC V70604;
DT 03-FEB-1999 (first entry)
DE cDNA encoding a murine multiple tumour suppressor 1E1-beta protein.
KW Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Mus sp.
PN US5843756-A.
PD 01-DEC-1998.
PF 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;

DR WPI; 99-044585/04.
PT Mouse multiple tumour suppressor gene segment - useful for primer
PT design
PS Example 8; Fig 14; 80pp; English.
CC The present sequence encodes murine multiple tumour suppressor 1E1-beta
CC (MTS1E1-beta) protein. Primers designed from the gene can be used to
CC design primers to detect abnormalities i.e. polymorphisms which may
CC predispose towards malignancies such as melanoma, leukaemia,
CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
CC thyroid, pancreas, uterus and kidneys.
SQ Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;

alignment_scores:

Quality: 445.00 Length: 85
Ratio: 5.235 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.824

alignment_block:

US-09-016-869A-6 x V70604 ..

Align seg 1/1 to: V70604 from: 1 to: 395

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140 ATGATGATGGGCAAGCTTCACGTACGACTCTTCGTCACTACGAGTGC 189

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
190 AGATTGCAACTCGAGGACCCCACTACCTTCTCCGCCCGGTGCAGGAC 239

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
240 CAGCGCGGAAGGCTTCTCGGACACGCTGGTGTGCTGCACGGGTACGG 289

51 AlaArgLeuAspValArgAspAlaTrrpGlyArgLeuProLeuAspLeuAl 67
|||||
290 GCTCGCTGGATGTCGCGATGCTCGGGTGGCTCCCTCCGCTCGACTTGC 339

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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340 CCAAGAGCGGGGACATCAAGACATCGTGCATATTGCGTTCCGCTGGGT 389

84 ySser 85
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seq_name: N_Geneseq_36:T00739

seq_documentation_block:

ID T00739 standard; DNA; 1187 BP.
AC T00739;
DT 08-MAY-1996 (first entry)
DE Multiple tumour suppressor 1 (MTS1) gene exon 2 contg. fragment.
KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
KW pancreas; breast; thyroid; exon 2; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT intron 1..191
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FT exon 192..498
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FT intron 499..1187
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PN WO9525813-A1.
PD 28-SEP-1995.
PF 17-MAR-1995; U03537.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.


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PR 18-MAR-1994; US-215086.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PA (MYRI-) MYRIAD GENETICS INC.
PA (UTAH ) UNIV UTAH RES FOUND.
PI Cannon-Albright LA, Kamb A, Skolnick MH;
DR WPI: 95-344626/44.
PT Detecting polymorphism associated with cancer pre-disposition - also
PT DNA, vectors and host cells e.g. for gene or protein replacement
PT therapy and drug screening
PS Claim 13; Pages 94-95; 148pp; English.
CC An individual can be diagnosed as having a predisposition to cancer
CC by detecting an alteration in the wild type multiple tumour
CC suppressor (MTS) gene, using gene probes which hybridise to exon 1
CC (T00737) or exon 2 (T00739) of the MTS1 gene. The above assay can
CC also be used in the diagnosis and prognosis of melanoma, lymphoma,
CC leukaemia and pancreas, breast and thyroid cancers, etc.
SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment_scores:
  Quality: 338.50      Length: 139
  Ratio: 3.319        Gaps: 2
  Percent Similarity: 73.381      Percent Identity: 52.518

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17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
245 GGACCCCACTGCGCCAGCCCGCCATCTCACCAGCCCGTGGACGACG 294

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
295 CTGCGCGGAGGGCTCTCTGACACGCTGCTGCTGCTGCTGCTGCTG 344

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
345 GCGCGGCTGGACGTCGCGAGTGCCTGGGGCGCTGCTGCGGACCTGG 394

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
395 TGAGGAGCTGGGCCATCGCGATGTCGACGCTACCTGCGCGCGCTGGG 444

84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly..... 97
445 GGGCACCAGAGGAGTAAACCATGCCGCTAGATGCCGCGAAGGTCCC 494

98 .....AsnValAlaGlnTh 102
495 TCAGGTGAGGACTGATGATCTGAGAAATTGTGACGCTGACGCTCCAAAG 544

102 rAspGlyHisSerPheSerSer.....SerThrProArgAlaLeuGluL 117
545 CTCAGAGCATTCATTTCCACAGCAGAAAGTTTCAGCCCGGAGACGAC 594

117 euArgGlyGlnSerGln 122
595 TCCGGTCTTGGCTCAG 611

seq_name: N_Genseq_36.V11240

seq_documentation_block:
  ID V11240 standard; DNA; 1187 BP.
  AC V11240;
  DT 15-JUL-1998 (first entry)
  DE Human MTS1 genomic DNA including exon 2.
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KW MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
KW familial melanoma locus; MLM; predisposition; ds.
OS Homo sapiens.
FH Key
FT CDS
FT Location/Qualifiers
FT 1..1187
FT /tag= a
FT /product= MTS1
FT /note= "partial coding region of multiple tumour
FT suppressor protein which is interrupted by
FT introns 1 and 2"
FT intron 1..191
FT /tag= b
FT /number= 1
FT exon 192..498
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FT /number= 2
FT intron 499..1187
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PN 14-APR-1998.
PE 07-JUN-1995; 487033.
PR 07-JUN-1995; US-487033.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 98-250421/22.
DR P-PSDB; W40524.
PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are
PT useful for the diagnosis of cancers related to MTS1E1-beta
PT mutation(s) and their treatment
PT Disclosure; Fig 6; 72pp; English.
PS This sequence encodes the human multiple tumour suppression protein,
CC MTS1, exon 2. The MTS gene locus is also referred to as the familial
CC melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line
CC mutations in MTS genes can be used in the diagnosis of predisposition to
CC cancers, e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma,
CC glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast,
CC thyroid, ovary, uterus, kidney, stomach and rectum.
SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment_scores:
  Quality: 338.50      Length: 139
  Ratio: 3.319        Gaps: 2
  Percent Similarity: 73.381      Percent Identity: 52.518

alignment_block:
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17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
245 GGACCCCACTGCGCCAGCCCGCCATCTCACCAGCCCGTGGACGACG 294

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
295 CTGCGCGGAGGGCTCTCTGACACGCTGCTGCTGCTGCTGCTGCTG 344

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
345 GCGCGGCTGGACGTCGCGAGTGCCTGGGGCGCTGCTGCGGACCTGG 394

seq_documentation_block:
  ID V11240 standard; DNA; 1187 BP.
  AC V11240;
  DT 15-JUL-1998 (first entry)
  DE Human MTS1 genomic DNA including exon 2.
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CC The present sequence represents part of intron 1, exon 2 and part
 CC of intron 2 for a human multiple tumour suppressor 1 (MTS1) gene. The
 CC MTS1 sequence is homologous to the corresponding murine gene.
 CC Primers designed from the gene can be used to design primers to
 CC detect abnormalities i.e. polymorphisms which may predispose towards
 CC malignancies such as melanoma, leukaemia, astrocytoma, lymphoma,
 CC glioma, as well as tumours of e.g. the breast, thyroid, pancreas,
 CC uterus and kidneys.
 SQ Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;

alignment_scores:
 Quality: 338.50 Length: 139
 Ratio: 3.319 Gaps: 2
 Percent Similarity: 73.381 Percent Identity: 52.518
 alignment_block:
 US-09-016-869A-6 x V70585 ..
 Align seg 1/1 to: V70585 from: 1 to: 1187

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 17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAsp 34
 |||||
 245 GGACCCCAACTGCGCCGACCCGCGCACTCTCACCAGCCCGTGCACGAC 294
 34 laAlaArgGluGlyPheLeuAspThrLeuValLeuHisGlySerGly 50
 |||||
 295 CTGCGCGGAGGGCTTCTGACACAGCTGGTGGTGGTGGTGGTGGTGG 344
 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
 |||||
 345 GCGCGGTGGAGCTGCGGATGCTGGGCGCTGCTGCCGCTGGACCTGGC 394
 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerIaGlyC 84
 |||||
 395 TGAGGAGCTGGCGCATCGCATGTCGACGGTACCTGCGCGCGCTGCGG 444
 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly..... 97
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 445 GGGCACCAGAGGAGTANCCATGCCCGCATAGATGCCCGGAGAGTCCC 494
 98
 495 TCAGGTGAGGACTGATGATCTGAGATTGTTGACCTGAGAGCTTCCRAAG 544
 102 rAspGlyHisSerPheSer.....SerThrProArgAlaLeuGluL 117
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 545 CTCAGAGCATTCATTTCCAGCAGACAGAAAGTTACGCCCGGAGACCAATC 594
 117 euArgGlyGlnSerGln 122
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 595 TCCGGTCTTGGCGTCAAG 611

seq_name: N_Geneseq_36:T00747

seq_documentation_block:
 ID T00747 standard; cDNA; 947 BP.
 AC T00747;
 DT 08-MAY-1996 (first entry)
 DE Multiple tumour suppressor 1 (MTS1) cDNA.
 KW Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
 KW predisposition; melanoma; leukaemia; lymphoma; prognosis;
 KW pancreas; breast; thyroid; ds.
 OS Homo sapiens.
 FH key Location/Qualifiers
 FT misc_feature 151
 FT /*tag= a
 FT /note= "splice site acceptor"
 FT misc_feature 458

FT /*tag= b
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WO9525813-Al.
 28-SEP-1995.
 17-MAR-1995; U03537.
 18-MAR-1994; US-214582.
 18-MAR-1994; US-215087.
 18-MAR-1994; US-215086.
 14-APR-1994; US-227369.
 01-JUN-1994; US-251938.
 (MYRI-) MYRIAD GENETICS INC.
 (UTAH) UNIV UTAH RES FOUND.
 Cannon-Albright LA, kamb A, Skolnick MH;
 WPI; 95-344626/44.
 Detecting polymorphism associated with cancer pre-disposition - also
 DNA, vectors and host cells e.g. for gene or protein replacement
 therapy and drug screening
 PS Disclosure: Pages 111-112; 148pp; English.
 CC An individual can be diagnosed as having a predisposition to cancer
 by detecting an alteration in the wild type multiple tumour
 suppressor (MTS) gene, using gene probes which hybridise to the MTS1
 cDNA T00747. The above assay can also be used in the diagnosis and
 prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and
 thyroid cancers, etc.
 SQ Sequence 947 BP; 207 A; 271 C; 273 G; 196 T;

alignment_scores:
 Quality: 332.00 Length: 122
 Ratio: 3.458 Gaps: 2
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 154 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTGCCACGGCGC 203
 17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAsp 34
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 204 GGACCCCAACTGCGCCGACCCGCGCACTCTCACCAGCCCGTGCACGACG 253
 34 laAlaArgGluGlyPheLeuAspThrLeuValLeuHisGlySerGly 50
 |||||
 254 CTGCGCGGAGGGCTTCTGACACAGCTGCTGGTGGTGGTGGTGGTGG 303
 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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 304 GCGCGGTGGACGTGCGCATGCTGCGGCGCTGCTGCCCGTGGACCTGGC 353
 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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 354 TGAGGAGCTGGCGCATCGCATGTCGACGGTACCTGCGCGCGCT.... 399
 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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 400GCGGGGGGCACC.....AGAGGCAGTAACCATGCC 429
 101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
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 117 uArgGlyGlnSerGln 122
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 480 GAGAGGCTCTGAGAAA 495
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 seq_documentation_block:
 ID T72311 standard; cDNA; 947 BP.


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Ratio: 5.252 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

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US-09-016-869A-6 x MMU79633 ..
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17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
|||||
54 AGATTCGAACCTGCGAGGACCCACTACCTTCTCCGCCGGTGCACGACG 103

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
104 CAGCGCGGGAAGGCTTCTGACACGCTGCTGGTGGTGCAGGGTCAAGG 153

51 AlaArgLeuAspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAl 67
|||||
154 GCTCGGCTGGATGTCGGGATGCTGGGTCGCTGGCTCGACTTGGC 203

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
204 CCAAGAGCGGGGACATCAAGACATCGTGGATATTGGCTTCCGCTGGGT 253

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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254 GGTCTTTGTTCGCTGGTGGTCTTTGTGTACCGCTGGGACGTCGCC 303

101 GlnThrAspGlyHisSerPheSerSerThrPro 112
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304 CAGACCGGCGCATAGCTTCAGCTCAAGCAGCGCC 339

seq_name: gb_ro:MMU79630

seq_documentation_block:
LOCUS MMU79630 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
gene, exon 2 and partial cds.
ACCESSION U79630
VERSION U79630.1 GI:4098147
KEYWORDS house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
JOURNAL Unpublished
REFERENCE
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
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BASE COUNT 54 a 100 c 112 g 73 t
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Quality: 579.00 Length: 112
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54 AGATTCGAACCTGCGAGGACCCACTACCTTCTCCGCCGGTGCACGACG 103

34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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104 CAGCGCGGGAAGGCTTCTGACACGCTGCTGGTGGTGCAGGGTCAAGG 153

51 AlaArgLeuAspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAl 67
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154 GCTCGGCTGGATGTCGGGATGCTGGGTCGCTGGCTCGACTTGGC 203

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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204 CCAAGAGCGGGGACATCAAGACATCGTGGATATTGGCTTCCGCTGGGT 253

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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254 GGTCTTTGTTCGCTGGTGGTCTTTGTGTACCGCTGGGACGTCGCC 303

101 GlnThrAspGlyHisSerPheSerSerThrPro 112
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304 CAGACCGGCGCATAGCTTCAGCTCAAGCAGCGCC 339

seq_name: gb_ro:MMU79630

seq_documentation_block:
LOCUS MMU79630 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
gene, exon 2 and partial cds.
ACCESSION U79630
VERSION U79630.1 GI:4098147
KEYWORDS house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
JOURNAL Unpublished
REFERENCE
AUTHORS Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
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104 CAGCGGGGAAGGCTCTCTGGACACGCTGGTGGTGCAGGGGTGACGG 153
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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154 GCTCGGCTGGATGCGCGATGCTGGGGTGCCTGCCCTCGACTTGGC 203
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
204 CCAAGACGCGGGACATCAAGACATCGTGGCATATTGCGTTCCGCTGGGT 253
84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
|||||
254 CGCTTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGACGTCGCC 303
101 GlnThrAspGlyHisSerPheSerSerSerThrPro 112
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304 CAGACCGACGGGCATAGCTTCAGCTCAAGCACGCC 339
seq_name: gb_ro:MMU79632
seq_documentation_block:
LOCUS MMU79632 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
gene, exon 2 and partial cds.
ACCESSION U79632

U79632.1 GI:4098151
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
Unpublished
JOURNAL 2 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Direct Submission
TITLE
JOURNAL Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
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TDGHSFSSSTP"
BASE COUNT 54 a 99 c 113 g 73 t
ORIGIN
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Quality: 578.00 Length: 112
Ratio: 5.207 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214
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Align seg 1/1 to: MMU79632 from: 1 to: 339
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seq_documentation_block:
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AC V53851;
DT 04-DEC-1998 (first entry)
DE Coding sequence 3 of the multiple tumour suppressor 1.
KW Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
KW somatic mutation; gene therapy; ds.
OS Homo sapiens.
PN US801236-A.
PD 01-SEP-1998.
PF 07-JUN-1995; 480810.
PR 07-JUN-1995; US-480810.
PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215086.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-227369.
PR 01-JUN-1994; US-251938.
PR 17-MAR-1995; WO-003316.
PA (MYRI-) MYRIAD GENETICS INC.
PI Kamb A;
DR WPI: 98-494842/42.
PT Nucleic acids based on multiple tumour suppressor, MTS, sequences -
PT useful as hybridisation probes, primers and recombinant production
PT of MTS in the diagnosis and treatment of cancers related to MTS
PT mutation(s)
PS Claim 1: Fig 17: 73pp; English.
CC This is the nucleotide sequence of the multiple tumour suppressor 1
CC (MTS-1) gene, used in the method of the invention. The MTS gene
CC is useful in the diagnosis and prognosis of human cancer, e.g. by
CC standard nucleic hybridisation techniques, of patient samples. The
CC mutated sequences are those that are present in somatic mutations
CC of the gene in cancers. The vectors can be used for gene therapy.
CC strategies to replace function of mutated protein in patients. These
CC can also be used to construct protein mimetics, also for therapeutic
CC strategies. In addition the expression constructs can also be used
CC for recombinant production of MTS. Recombinant MTS can be used to
CC screen for drugs to be used for cancer therapy, and the protein
CC itself may also be used to restore MTS function in a cell.
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

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  Quality: 332.00      Length: 122
  Ratio: 3.458        Gaps: 2
Percent Similarity: 78.689 Percent Identity: 57.377

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154 ATGATGATGGCGAGCGCCGAGTGGCGGAGTGTCTGCTCCACGGCGC 203

17 aAspSerAsnCysGluAspProThrPheSerArgProValHisAspA 34
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204 GGACCCCACTGCGCCGACCCCGCCACTCTCACCAGCCGCTGCACGACG 253
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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254 CTGCCCGGAGGGCTTCTCTGACACGCTGTGTGCTGCACCGGCGCGG 303

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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304 GCGGGCTGGACGTGCGCATGCTGGGGCGCTCTGCCGTGGACCTGGC 353

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValala 100
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400 .....GCGGGGGGACC.....AGAGGCAGTAACCATGCC 429

101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
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430 CGCATAGTCCCGGGAAGTCCCTCAGACATCCCGATTGAAGAACCACCA 479

117 uArgGlyGlnSerGln 122
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seq_name: N_Geneseq_36:V70615
seq_documentation_block:
ID V70615 standard; cDNA; 947 BP.
AC V70615;
DT 03-FEB-1999 (first entry)
DE CDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.
KW Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
OS Homo sapiens.
FH Key
FH Location/Qualifiers
FT misc_feature 151
FT /*tag= a
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FT US5843756-A.
PN 01-DEC-1998.
PD 28-JUL-1995; 058735.
PR 28-JUL-1995; US-508735.
PR 07-JUN-1995; US-487033.
PA (MYRI-) MYRIAD GENETICS INC.
PI Jiang P, Kamb A, Stone S;
PI WPI: 99-04585/04.
DR Mouse multiple tumour suppressor gene segment - useful for primer
DR design
PT Disclosure; Fig 17: 80pp; English.
PS The present sequence represents the cDNA sequence for a human multiple
PS tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene
PS can be used to design primers to detect abnormalities i.e. polymorphisms
PS which may predispose towards malignancies such as melanoma, leukaemia,
PS astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
PS thyroid, pancreas, uterus and kidneys.
SQ Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;

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alignment_scores:
  Quality: 332.00      Length: 122
  Ratio: 3.458        Gaps: 2
Percent Similarity: 78.689 Percent Identity: 57.377

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alignment_block:
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US-09-016-869A-6 x V70615 ..
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34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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254 CTGCCCGGAGGGCTTCCTGGACACGCTGGTGTCTGCACCGGCCCGGG 303
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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304 GCGCGGCTGGAGTCGCGCATCCCTGGGCGCGTCTGCCCGTGGACCTGGC 353
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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354 TGAGAGCTGGGCCATCGGATGTGCGACGGTACCTGCGCGGGGT.... 399
84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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400 .....GCGGGGGCACCC.....AGAGGCAGTAACCATGCC 429
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OM of: US-09-016-869A-6 to: Issued_Patents_NA.* out_format : pfs
Date: Jul 21, 2000 8:07 AM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL-frame+ p2n.model -DEV-xlp
-Q/cgn2_1/USPTO_Spool/US09016869/runat_20072000_083606_16091/app_query.fasta_1.598
-DB-Issued_Patents_NA -QPMT-fastcap -SUFFIX=rr1 -GAPOP=12.000
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Search information block:
Query: US-09-016-869A-6
Query length: 125
Database: Issued_Patents_NA.*
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; Sequence 44, Application US/08508735
; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jhang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Inhen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORGANISM: Mus musculus
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; Patent No. 5723313
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell
; TITLE OF INVENTION: Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,975
; FILING DATE: 28-SEP-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0590000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
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; US-08-534-975-1

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Ratio: 5.264 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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; Sequence 1, Application US/08954470
; Patent No. 5876965
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 5876965el Regulator of the
; TITLE OF INVENTION: Mammalian Cell Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/954,470
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/534,975
; FILING DATE: 28-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0656.0590000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..548
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; US-08-954-470-1

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17 aAspSerIasnCysGluAspProThrThrPheSerArgProValHisAspA 34
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34 IaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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336 CAGCCGGGAAGGCTCTCTGGACACGCTGGTGTCTCCGCGCGGTGACGG 385

51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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386 GCTCGGCTGGATGCGCGATGCGTGGGTGCGCTGCCGCTCGACTTGGC 435

67 agInGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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84 ysSerLeuCysSerAlaGlyTyrPheSerLeuCysThrAlaGlyAsnValAla 100
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101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
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; Sequence 1, Application US/09129855A
; Patent No. 6046032
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 6046032el Regulator of the Mammalian
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue Sule 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/129,855A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/954,470
; FILING DATE: 20-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/534,975
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-023 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..548
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; NAME/KEY: CDS
; LOCATION: 43..551
; US-09-129-855A-1

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seq_documentation_block:
; Sequence 5, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306.511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

; LOCATION: 213...587
; US-08-306-511A-5

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Ratio: 5.264 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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263 AGATTGGAACCTGGCAGGACCCACTACTCTCCCGCCGGTGCACGAGC 312
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51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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363 GCTCGGCTGATGTGCGGATGCTCGCTGGGTGCGCTGCCGCTGCACTTGGC 412
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67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
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413 CCAAGACGGGGACATCAAGACATCGTGCATATTTGCGTTCCGCTGGGT 462
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84 ySerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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463 GCTCTTTGTTCGCTGGGTGGTGTCTTTGTGTACCGCTGGGAACGTCGCC 512
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101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
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513 CAGACCGACGGGATAGCTTCAGCTCAAGCACGCCAGGCGCTGGAAC 562
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seq_documentation_block:
; Sequence 5, Application US/08893274
; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893.274
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
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117 FILING DATE: 15-JULY-1997
118 CLASSIFICATION: 800
119 PRIOR APPLICATION DATA:
120 FILING DATE: 14-SEPTEMBER-1994
121 PRIOR APPLICATION NUMBER: US 08/306,511
122 FILING DATE: 14-SEPTEMBER-1994
123 PRIOR APPLICATION DATA:
124 FILING DATE: 25-MAY-1994
125 PRIOR APPLICATION NUMBER: US 08/248,812
126 FILING DATE: 25-MAY-1994
127 PRIOR APPLICATION DATA:
128 FILING DATE: 14-APRIL-1994
129 PRIOR APPLICATION NUMBER: US 08/227,371
130 FILING DATE: 18-NOVEMBER-1993
131 PRIOR APPLICATION DATA:
132 FILING DATE: 18-NOVEMBER-1993
133 PRIOR APPLICATION NUMBER: US 07/991,997
134 FILING DATE: 17-DECEMBER-1992
135 PRIOR APPLICATION DATA:
136 FILING DATE: 16-OCTOBER-1992
137 PRIOR APPLICATION NUMBER: US 07/963,308
138 FILING DATE: 16-OCTOBER-1992
139 ATTORNEY/AGENT INFORMATION:
140 NAME: Vincent, Matthew P.
141 REGISTRATION NUMBER: 36,709
142 REFERENCE/DOCKET NUMBER: MIV-071.09
143 TELECOMMUNICATION INFORMATION:
144 TELEPHONE: (617) 832-1000
145 TELEFAX: (617) 832-7000
146 INFORMATION FOR SEQ ID NO: 5:
147 SEQUENCE CHARACTERISTICS:
148 LENGTH: 853 base pairs
149 TYPE: nucleic acid
150 STRANDEDNESS: both
151 TOPOLOGY: linear
152 MOLECULE TYPE: cdna
153 FEATURE:
154 NAME/KEY: CDS
155 LOCATION: 213..587
156 US-08-893-274-5

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157 Quality: 658.00 Length: 125
158 Ratio: 5.264 Gaps: 0
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; Sequence 5, Application US/08581918A
; Patent No. 6043030
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Elliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPad
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; APPLICATION NUMBER: US/08/581,918A
; FILING DATE: 02-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/497,214
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1299
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
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; NAME/KEY: CDS
; LOCATION: 213..587
; US-08-581-918A-5

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34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
363 GCTCGGCTGGATGTCCGCGATGCCCTGGGGTGCCTTCGCCCTCGACTTGGC 412

67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
413 CCAAGAGCGGGACATCAAGACATCGTCGCATATTTCGCTCCGCTGGGT 462

84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
463 GCTCTTTGTGTTCGCGTGGGTGCTCTTTGTGTACCGCTGGGAACGTCGCC 512

101 GlnThrAspGlyHisSerPheSerPheSerSerSerThrProArgAlaLeuGluLe 117
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; Sequence 5, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
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; PRIORITY APPLICATION DATA:
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; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
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; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,610
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 857 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; Patent No. 5624819
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
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; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; FILING DATE: 07-JUN-1995
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; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
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; APPLICATION NUMBER: US 08/251,938
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 base pairs
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; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
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; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-C
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APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
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TELEFAX: 202-962-8300
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; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
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; TELEPHONE: 202-962-8300
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; Patent No. 5843756
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; FILING DATE:
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; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 395 base pairs
; TYPE: nucleic acid
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; ANTI-SENSE: NO
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; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; TITLE OF INVENTION: GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
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; FILING DATE: 17-MAR-1995
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; FILING DATE: 01-JUN-1994
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; FILING DATE: 18-MAR-1994
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; FILING DATE: 18-MAR-1994
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; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
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; SEQUENCE CHARACTERISTICS:

; LENGTH: 395 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; ANTI-SENSE: NO
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; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
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APPLICATION NUMBER: US 08/227,369
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APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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About: Results were produced by the GenCore software, version 4.5,
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gb_est9:AA557137	-	221.00	418.10	1.8e-14	599	AA557137 n174b05.s1 NCI_CGAP_Bd
gb_est14:AA946565	-	218.00	413.47	3.3e-14	531	AA946565 qd49e06.s1 NCI_CGAP_Ki
gb_est16:AI091727	-	207.00	393.77	4.2e-13	450	AI091727 ow52g04.x1 Soares_NSF
gb_est13:AA877595	-	200.00	392.07	5.2e-13	533	AA877595 n07f06.s1 NCI_CGAP_Cd
gb_est13:AA903110	-	198.00	374.32	5.1e-12	548	AA903110 ok52b03.s1 NCI_CGAP_Le
gb_est25:AI818660	+	185.00	350.71	1.0e-10	465	AI818660 wh89c11.x1 NCI_CGAP_Lu
gb_est25:AI798040	+	180.00	338.36	5.1e-10	606	AI798040 wh89g12.x1 NCI_CGAP_Cd
gb_est19:AI337358	-	180.00	337.07	6.0e-10	689	AI337358 tb98f09.x1 NCI_CGAP_Cd
gb_est21:AI499733	+	175.00	328.95	1.7e-09	588	AI499733 tm91g12.x1 NCI_CGAP_Bd
gb_est15:AI057178	+	172.50	325.28	2.7e-09	522	AI057178 oy78b02.x1 NCI_CGAP_Cd
gb_est24:AI690174	+	172.50	323.79	3.3e-09	606	AI690174 tx33a05.x1 NCI_CGAP_Lu
gb_est38:AW169901	+	171.50	323.13	3.6e-09	533	AW169901 x134d12.x1 Soares_NFL
gb_est1:AA055664	-	168.00	320.17	5.3e-09	441	AA055664 z175f06.s1 Stratagene
gb_est23:AI656826	+	169.00	317.84	7.1e-09	557	AI656826 tj54c09.x1 NCI_CGAP_Gd
gb_est1:AA051504	+	169.00	314.90	1.0e-08	747	AA051504 m53e11.rl Soares_mous
gb_est55:W98530	+	169.00	314.29	1.1e-08	794	W98530 mg21d06.rl Soares_mous
gb_est52:R77517	+	168.50	322.34	4.0e-09	322	R77517 y179h08.s1 Soares placed

gb_est24:AI703354 + 168.50 316.17 8.8e-09 597 | AI703354 wd93c07.x1 NCI_CGAP
gb_est1:AA051335 + 167.50 313.11 1.5e-08 668 | AA051335 mj40b12.rl Soares m
gb_est26:AI869175 - 167.00 313.85 1.2e-08 563 | AI869175 w150c04.x1 NCI_CGAP
gb_est18:AI280899 - 166.00 311.99 1.5e-08 558 | AI280899 qk47d01.x1 NCI_CGAP
seq_name: gb_est26:AI871381
seq_documentation_block: 590 bp mRNA EST 07-MAR-2000
LOCUS AI871381
DEFINITION w18d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3',
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION AI871381
VERSION AI871381.1 GI:5545430
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 590)
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
Location/Qualifiers
1..590
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2431317"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pTTT3D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; lstr
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAAGTGGAGCGCCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pTTT3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 114 a 158 c 179 g 139 t
ORIGIN
alignment_scores:
Quality: 332.00 Length: 122
Ratio: 3.458 Gaps: 2
Percent Similarity: 78.689 Percent Identity: 57.377
alignment_block:
US-09-016-869A-6 x AI871381/rev ..
Align seg 1/1 to reverse of: AI871381 from: 1 to: 590
1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17


```
34 laalaarggluglypheleuaspthrleuvalvalleuHisGlySerGly 50
|||||
449 CTGCCGGGAGGCTTCCTGGACAGCTGGTGTGTGCACCGGCGCGG 400
|||||
51 AlaArgLeuAspValargaspalarpglyArgLeuProLeuAspLeuAl 67
|||||
399 GCGCGGCTGGAGTGGCGATCGCTGGGCGCTGTGCGCGTGGACCTGGC 350
|||||
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
349 TGAGGAGCTGGCCATCGCATGTGCACGGTACCTGGCGCGGT.... 304
|||||
84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
|||||
303 .....GCGGGGGGCACC.....AGAGGCAGTAACCATGCC 274
|||||
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
|||||
273 CGCATAGATGCGCGGAGAGGTCCCTCAGACATCCCGGATTGAAGAACA 224
|||||
117 uArgGlyGlnSerGln 122
|||||
223 GAGAGGCTCTGAGAAA 208
|||||
seq_name: gb_est19:AI363262

seq_documentation_block:
LOCUS AI363262 708 bp mRNA EST 16-FEB-1999
DEFINITION q556f03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3'
similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains
LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION AI363262
VERSION AI363262.1 GI:4114883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 708)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
TITLE (CGAP/BTGP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 872 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 394.
FEATURES
source
1..708
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2016029"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
```

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 137 a 210 c 219 g 140 t 2 others
ORIGIN

alignment_scores:
Quality: 323.00 Length: 122
Ratio: 3.400 Gaps: 2
Percent Similarity: 77.869 Percent Identity: 56.557

alignment_block:

US-09-016-869A-6 x AI363262/rev ..

Align seg 1/1 to reverse of: AI363262 from: 1 to: 708

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1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
|||||
534 ATGATGATGCAAGCGCCGAGTGGCAAGCTGCTGCTCCCGGCGC 485
|||||
17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
|||||
484 GGAGCCCACTGCGACGACCCGCCAACTCTCACCCGACCGCTGCACGACG 435
|||||
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||
434 CTGCCGGGAGGCTTCCTGGACAGCTGGTGTGTGCACCGGCGCGG 385
|||||
51 AlaArgLeuAspValargaspalarpglyArgLeuProLeuAspLeuAl 67
|||||
384 GCGCGGCTGGACGTGGCGCATGCTGCGGCGCTGCGCGTGGACCTGGC 335
|||||
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||
334 TGAGGAGCTGGCCATCGCATGTGCACGGTACCTGGCGCGGCT.... 289
|||||
84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
|||||
288 .....GCGGGGGGCACC.....AGAGGCAGTAACCATGCC 259
|||||
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
|||||
258 CGCATAGATGCGCGGAGAGTCCCTCAGACATCCCGGATTGAAGAACA 209
|||||
117 uArgGlyGlnSerGln 122
|||||
208 GAGAGGCTCTGAGAAA 193
|||||
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seq_name: gb_est17:AI198233

seq_documentation_block:

LOCUS AI198233 579 bp mRNA EST 02-DEC-1998
DEFINITION q155d12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI198233

VERSION AI198233.1 GI:3750839

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 579)

AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGP), Tumor Gene Index

JOURNAL Unpublished (1998)

COMMENT Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 729 Std Error: 0.00
 Seq primer: -40Up from Gibco
 High quality sequence stop: 459.
 Location/Qualifiers

FEATURES

source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1860407"
 /clone_lib="NCI CGAP Brn25"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAACTGAAGTGGAGCGCGCATAGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
 BASE COUNT 113 a 158 c 177 g 130 t 1 others
 ORIGIN

alignment_scores:
 Quality: 315.00 Length: 122
 Ratio: 3.351 Gaps: 2
 Percent Similarity: 77.049 Percent Identity: 55.738

alignment_block:
 US-09-016-869A-6 x A1198233/rev ..

Align seg 1/1 to reverse of: A1198233 from: 1 to: 579

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1 MetMetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17
|||||.....:.....:.....:.....:.....:.....:
549 ATGATGATGGCGAGCGCGCGAGTGGCGAAGCTGCTGCTCCACAGCG 500
|.....:.....:.....:.....:.....:.....:
17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
|||||.....:.....:.....:.....:.....:.....:
499 GAAGCCCAACTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||.....:.....:.....:.....:.....:.....:
449 CTGCGCGGAGGGCTTCCTGGACACGCTGGTGTGTGCACCGCGGCGG 400
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
|||||.....:.....:.....:.....:.....:.....:
399 GCGCGGCTGGACGTGGCGATGCTGCGGCGCGCTGCTGCGGACCTGGC 350
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
|||||.....:.....:.....:.....:.....:.....:
349 TGAGAGCTGGGCCATCGCGATGTCGACGGTACCTGCGCGCGGCT.... 304
84 ySerLeuCysSerAlaGlyTyrPsrLeuLeuCysThrAlaGlyAsnValAla 100
|||||.....:.....:.....:.....:.....:.....:
303 .....GCGGGGGGACCC.....AGAGGACGTAACCATGCC 274
101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
::: |||::: ::: |||::: |||
273 CGCATAGATGCGCGGAAGGTCCCTCAGACATCCCGGATTGAAGAACCAC 224
117 uArgGlyGlnSerGln 122
|||||.....:.....:

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223 GAGAGGCTCTGAGAA 208

seq_name: gb_gss7:AQ496105

seq_documentation_block: 614 bp DNA GSS 28-APR-1999
 LOCUS AQ496105 HS_5075_Al_F12_T7 RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate-651 Col-23 Row-K, genomic survey sequence.
 ACCESSION AQ496105

VERSION AQ496105.1 GI:4696228

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 614)

REFERENCE

AUTHORS

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and Hood,L.

TITLE

JOURNAL

MEDLINE

COMMENT

On Dec 15, 1999 this sequence version replaced gi:4575297.
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887

Email: jwallaceu.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://inforesgen.com>). BAC end web Server: <http://www.htsc.washington.edu>
 Plate: 651 row: K column: 23
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 614.

FEATURES

source

Location/Qualifiers

1..614

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-651 Col-23 Row-K"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 117 a 182 c 171 g 133 t 11 others
 ORIGIN

alignment_scores:

Quality: 312.00 Length: 81

Ratio: 4.274 Gaps: 0

Percent Similarity: 90.123 Percent Identity: 72.840

alignment_block:

US-09-016-869A-6 x AQ496105 ..

Align seg 1/1 to: AQ496105 from: 1 to: 614

1 MetMetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17

|||||.....:.....:.....:.....:.....:.....:
297 ATGATGATGGCGACCGCGCGAGTGGCGGAGCTGCTGCTCCACGGGC 346

17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34

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1::: ||||| - |||||:::|||||:::|||||:::|||||:::|||||
347 GGAGCCCACTGGCGACCCGCCACTCTCACCCGACCGCTGCACGACG 396
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
397 CTGCCGGGAGGCTTCTTGGACACACTGGTGTGCTGCACCGGCGGG 446
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
447 GCGGGCTGCAGCTGCCTATGCTGGCGCGCTCTGCCGTGGACCTGCG 496
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSer 81
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
497 TGAGGAGCTGGGCGCATCTCGATGTTACACGGTACCTGCGCGCG 539

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seq_name: gb_est25:AI765096

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seq_documentation_block: 774 bp mRNA EST 21-DEC-1999
LOCUS AI765096
DEFINITION w148b08.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2393463 3'
similar to TR:Q13399 Q13399 HYPOPHETICAL 18.1 KDA PROTEIN ;contains
LTR9.b3 MER22 repetitive element ;, mRNA sequence.
ACCESSION AI765096
VERSION AI765096.1 GI:5231605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
Location/Qualifiers
1..774
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2393463"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/Note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site: 1; Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
153 a 220 c 221 g 179 t 1 others

```

```

BASE COUNT
ORIGIN
alignment_scores:
Quality: 312.00 Length: 120
Ratio: 3.429 Gaps: 3.

```

FEATURES

```

source
1..774
seq_documentation_block: 580 bp mRNA EST 15-FEB-1999
LOCUS AI362049
DEFINITION qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION AI362049
VERSION AI362049.1 GI:4113670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 580)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
Seq primer: -40UP from Gibco

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Percent Similarity: 75.833 Percent Identity: 57.500
alignment_block:
US-09-016-869A-6 x AI765096/rev ..
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1 MetMetMetGlyAsnValHisValAlaLeuLeuLeuAsnTyrGlyAl 17
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584 ATGATGATGGCAGCGCCGAGTGGCGAGCTGCTGCTCCACGGCGC 535
17 aspSerAsnCysGluaspProThrThrPheSerArgProValHisaspA 34
::: ||| |||||:::|||||:::|||||:::|||||:::|||||
534 GGAGCCCAATTGGGCGCGACCCGCCACTTTCACCCGAACCGTGCACGACG 485
34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
484 CTGCCGGGAGGCTTCTTGGACACGCTGGTGTGCTGCACCGGCGGG 435
51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
434 GCGCGGCTGGACGTGCGCAATGCTGGGCGCTGCTGCCGTGGACCTGGC 385
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
::: ||| |||||:::|||||:::|||||:::|||||:::|||||
384 TGAGGAGCTGGGCGCATCTCGATGTTACCGCGGCTACCTGCGCGCGCT... 339
84 ysSerLeuCySerAlaGlyTrpSerLeuCyThrAlaGly...AsnVal 99
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
338 .....TCGGGGGGC.....ACCAGAGCGAGTAACCAT 312
100 AlaGlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGl 116
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
311 GCCGCATAAATCGCGGAAGGTCCCTCAGACATCCCGCATTTAAAGAA 262
116 uLeuArgGly 119
: |||||
261 CCAAGAGGG 252
seq_name: gb_est19:AI362049
seq_documentation_block: 580 bp mRNA EST 15-FEB-1999
LOCUS AI362049
DEFINITION qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; mRNA sequence.
ACCESSION AI362049
VERSION AI362049.1 GI:4113670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 580)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
Seq primer: -40UP from Gibco

```


us-09-016-869a-6.rst

2000

ACCESSION AL869A
VERSION 1
LeuArgSerAlaGlyCysSerLeuCysSerAlaGlyT 91
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TACCTGGCGGGCT GCGGGG 297
euCysThrAlaGlyAsnValAlaGlnThrAspGlyHisSerPhe 107
:|||||
:|||||
CACC.....AGAGGAGATACCATCGCGCATAGATCCCGGAAGGT 253

108 SerSerThrProArgAlaLeuGluLeuArgGlyGlnSerGln 122
:|||||
:|||||
252 CCTCAGACATCCCGATTGAACACAGAGAGGCTCTGAGAA 208

seq_name: gb_est25:AI817709

seq_documentation_block: 729 bp mRNA EST 21-DEC-1999
LOCUS AI817709 NCI-CCAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3'
DEFINITION WK25c11.x1 NCI-CCAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA
sequence.

ACCESSION AI817709 GI:5436788

VERSION AI817709

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 729)

AUTHORS NCI/NINDS-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index

JOURNAL Unpublished (1998)

COMMENT On Apr 7, 1998 this sequence version replaced gi:3035534.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 848 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 468.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2413364"
/clone_lib="NCI-CCAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTATCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 141 a 214 c 256 g 143 t 5 others
ORIGIN

alignment_scores:
Quality: 308.00 Length: 119
Ratio: 3.348 Gaps: 2
Percent Similarity: 77.311 Percent Identity: 55.462

alignment_block:
US-09-016-869a-6 x AI817709/rev ..
Align seg 1/1 to reverse of: AI817709 from: 1 to: 729

4 GlyAsnValHisValAlaLeuLeuAsnTyrGlyAlaAspSerAs 20
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:|||||
540 GCGAGCGCGAAGTGGCGGAGCTGCTGCTCCACGGCGGAGCCAA 491
|||||

20 CysGluAspProThrThrPheSerArgProValHisAspAlaAArg 37
|||||
:|||||
490 CTGCGCCGACGCCCACTCTCACCAGCCCGTGCACGCTGCCCGGG 441
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37 LuGlyPheLeuAspThrLeuValValLeuHisGlySerGlyAlaAArg 53
|||||
:|||||
440 AGGGCTTCTGTGACACGCTGTGTGTGTGTGACCCGGCGGGCGCGCTG 391
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54 AspValArgAspAlaTyrGlyArgLeuProLeuAspLeuAArgGln 70
|||||
:|||||
390 GACGTGCGGATCGCTGGGGCGCTGCTGCCGTGGACCTGGCTGAGGAGCT 341
|||||

70 GglyHisGlnAspIleValArgTyrLeuArgSerAlaGlyCysSerLeu 87
|||||
:|||||
340 GGGCCATCGGATGTGCGACGACTGCGCGCGGCT 304
|||||

87 YsSerAlaGlyTyrSerLeuCysThrAlaGlyAsnValAlaGlnThr 103
|||||
:|||||
303GCGGGGGGCGCCAGAGGCGAGTACCATGCCCGCATAGAT 265
|||||

104 GlyHisSerPheSerSerThrProArgAlaLeuGluLeuArgGlyGln 120
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:|||||
264 GCGCGGAGAGTCCCTCAGACATCCCGATTGAACACAGAGAGGCTC 215
|||||

120 nSerGln 122

214 TGAGAAA 208

seq_name: gb_est23:AI638416

seq_documentation_block: 528 bp mRNA EST 14-DEC-1999
LOCUS AI638416 NCI-CCAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
DEFINITION TT31903.x1 NCI-CCAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
; contains LTR9.B3 TAR1 repetitive element ;, mRNA sequence.

ACCESSION AI638416 GI:4690650

VERSION AI638416

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 528)

AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 462.

14:40 2000

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545 ATGATGATGGCGACGCCCGAGTGGCGGAGCTGCTGCTCCACGGCGC 496
17 aaspsersascysgluaspprothrthrpheserargprovalhisaspa 34
495 GGAGCCCACTG.CCCGACCCCACTCTACCCGACCCGTCGACGACG 447
34 laalaarggluglypheleuaspprothrthrpheserargprovalhisaspa 50
446 CTGCGCGGAGGGCTTCCTGGACACGCTGGTGGTGTGCACCGGCGGG 397
51 Alaargleuaspsvalaraspalatrppglyargleuproleuaspleu 67
396 GCGCGCTGGACGTCGCGATGCGTGGCGCGCTGCTGCCGTCGACCTGGC 347
67 aglngluargglyhisglinspalevalargtyrleuargseralaglyc 84
346 TGAGGAGCTGGCCATCGCGATGTGCGACGCTGCTGCTGCTGCTGCTG 301
84 ysserleucysseralaglytrpserleucysvalargtyrleuargser 100
300 .....GCGGGGGGCGACCC.....AGAGGCGAGTAAACATGCC 271
101 Glnthrargglyhisserpheserargprovalhisaspa 117
270 CGCATAGATGCGCGGAGTCCCTCAGACATCCCGGATTAAGAACCA 221
117 uargglylnsergln 122
220 GAGAGCTCTGAGAAA 205
seq_name: gb_est13:AA909181
seq_documentation_block: 526 bp mRNA EST 10-JUN-1998
LOCUS AA909181
DEFINITION IMAGE:1523215 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE
REGULATOR BETA FORM ; mRNA sequence.
ACCESSION AA909181
VERSION AA909181.1 GI:3048586
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On Apr 7, 1998 this sequence version replaced gi:3034533.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 581 Std Error: 0.00
Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 398.
Location/Qualifiers
1..526
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/db_xref="taxon:9606"
/clone="IMAGE:1523215"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site: 1: Not 1; Site: 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP.GCBI) were mixed, and ss circles were used as
vectors. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same library (clones 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bernaldo.
BASE COUNT 112 a 158 c 169 g 124 t
ORIGIN
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Quality: 299.00 Length: 122
Ratio: 3.191 Gaps: 2
Percent Similarity: 77.049 Percent Identity: 56.557
alignment_block:
US-09-016-869A-6 x AI954684/rev ..
Align seg 1/1 to reverse of: AI954684 from: 1 to: 563
1 MetMetMetClyAsnValHisValAlaAlaLeuLeuAsnTyrGlyAl 17
|||||
1 MetMetMetClyAsnValHisValAlaAlaLeuLeuAsnTyrGlyAl 17
|||||
```


